

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw mode¹

Run on: March 11, 2004, 20:36:42 ; Search Time 2283.3 Seconds
(without alignments)
1386.917 Million cell updates/sec

Title: US-10-003-035-74
Perfect score: 90
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Scoring table: IDENTITY_NTC
Gapop 10.0 , Gapext 1.0

Searched: 37577330 seqs, 17593059518 residues

Total number of hits satisfying chosen parameters: 75154660
Maximum Match 0%
Maximum Match 100%
Listing first 45 summaries

Pending Patents_NA_Main:*

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33: /cggn2_6/_ptodata/2/pna/US098A_COMB.seq: *
34: /cggn2_6/_ptodata/2/pna/US098B_COMB.seq: *
35: /cggn2_6/_ptodata/2/pna/US098C_COMB.seq: *
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42: /cggn2_6/_ptodata/2/pna/US100A_COMB.seq: *
43: /cggn2_6/_ptodata/2/pna/US100B_COMB.seq: *

¹pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES


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ZIP: 07065
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS MS-DOS
; SOFTWARE: Patentent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/207,526
; APPLICATION NUMBER: US/08/207,526
; FILING DATE: 2003-03-17
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Bencen, Gerard H
; REGISTRATION NUMBER: 35,746
; REFERENCE/DOCKET NUMBER: 19188
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3901
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 119 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-10-280-915-4
; OTHER INFORMATION: DNA encoding gp120 signal peptide
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Best Local Similarity 100.0%; Pred. No. 7.7e-18; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
Qy 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
Db 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
; RESULT 4
; Sequence 74, Application US/10286332A
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
; FILE REFERENCE: 22488-738
; CURRENT APPLICATION NUMBER: US/10/286,332A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOs: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 90
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE: OTHER INFORMATION: DNA encoding gp120 signal peptide
; US-10-288-332A-74
Query Match 100 0%; Score 90; DB 48; Length 90;
Best Local Similarity 100.0%; Pred. No. 7.7e-18; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
Qy 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
Db 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
; RESULT 5
; Sequence 58, Application US/08207526
; GENERAL INFORMATION:
; APPLICANT: Shiver, John W
; APPLICANT: Liu, Margaret A
; TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue, P.O. Box 2000
; CITY: Rahway
; COUNTRY: United States of America
Query Match 100.0%; Score 90; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
PCT-US02-35112-41
; ORGANISM: Human immunodeficiency virus type 1
; SEQ ID NO 41
; LENGTH: 486
; TYPE: DNA
; PCT-US02-35112-41
Query Match 100 0%; Score 90; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
Qy 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
Db 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
; RESULT 6
; Sequence 41, Application PC/TUS0235112
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-740
; CURRENT APPLICATION NUMBER: PCT/TUS02/35112
; CURRENT FILING DATE: 2003-11-01
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOs: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 486
; TYPE: DNA
; PCT-US02-35112-41
Query Match 100 0%; Score 90; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
Qy 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
Db 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
; RESULT 7
; Sequence 59, Application US/08207526
; GENERAL INFORMATION:
; APPLICANT: Perry, Helen C
; APPLICANT: Liu, Margaret A
; TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue, P.O. Box 2000
; CITY: Rahway
; COUNTRY: New Jersey
Query Match 100 0%; Score 90; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
Qy 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
Db 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
; RESULT 8
; Sequence 60, Application US/08207526
; GENERAL INFORMATION:
; APPLICANT: Liu, Margaret A
; TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue, P.O. Box 2000
; CITY: Rahway
; COUNTRY: New Jersey
Query Match 100 0%; Score 90; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
Qy 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
Db 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
; RESULT 9
; Sequence 61, Application US/08207526
; GENERAL INFORMATION:
; APPLICANT: Liu, Margaret A
; TITLE OF INVENTION: COORDINATE IN VIVO GENE EXPRESSION
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: 126 Lincoln Avenue, P.O. Box 2000
; CITY: Rahway
; COUNTRY: New Jersey
Query Match 100 0%; Score 90; DB 1; Length 486;
Best Local Similarity 100.0%; Pred. No. 1.e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0;
Qy 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60
Db 1 ATGAGGTGAGGAGAATAAGCACTTGGAGATGGGATCAGATGGGACCATG 60

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RESULT 9
US-10-286-332A-41
; Sequence 41, Application US/10286332A
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Danher
 ; TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
 ; FILE REFERENCE: 2488-738
 ; CURRENT APPLICATION NUMBER: US/10/286,332A
 ; CURRENT FILING DATE: 2003-03-17
 ; PRIOR APPLICATION NUMBER: US 09/585,599
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US01/18238
 ; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: US 10/003,035
 ; PRIOR FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 41
 ; LENGTH: 486
 ; TYPE: DNA
 ; ORGANISM: Human immunodeficiency virus type 1
 US-10-286-332A-41

Query Match 100.0%; Score 90; DB 43; Length 486;
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGAGGAAATAATCAGCACTTGAGATGGGGTGGAGATGGGGCACCATG 60
 Db 1 ATGAGATGAGGAAATAATCAGCACTTGAGATGGGGTGGAGATGGGGCACCATG 60

Qy 61 CTCCCTGGATGTGATGATCTGATGCTGATGCT 90
 Db 61 CTCCCTGGATGTGATGATCTGATGCT 90

RESULT 10
US-08-628-686-66
; Sequence 66, Application US/08628686
 ; GENERAL INFORMATION:
 ; APPLICANT: Tabler, Martin
 ; TITLE OF INVENTION: ASYMMETRIC HAMMERHEAD RIBOZOMES AND
 ; NUMBER OF SEQUENCES: 116
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hardaway Law Firm
 ; STREET: P.O. Box 10107 Federal Station
 ; CITY: Greenville
 ; STATE: SC
 ; COUNTRY: USA
 ; ZIP: 29603-0107
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC Compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/628,686
 ; FILING DATE: 30-MAY-1996
 ; CLASSIFICATION: 514
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/EP94/03391
 ; FILING DATE: 14-OCT-1994
 ; APPLICATION NUMBER: EP EP93/02853
 ; FILING DATE: 15-OCT-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hardaway III, John B.
 ; REGISTRATION NUMBER: 26,554
 ; REFERENCE/DOCKET NUMBER: RPE-03
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 864-233-6700

RESULT 6
US-10-280-915-41
; Sequence 41, Application US/10280915
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Danher
 ; TITLE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADENOVIRUS
 ; FILE REFERENCE: 22499-741
 ; CURRENT APPLICATION NUMBER: US/10/280,915
 ; CURRENT FILING DATE: 2002-10-24
 ; PRIOR APPLICATION NUMBER: US 09/585,599
 ; PRIOR FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: PCT/US01/18238
 ; PRIOR FILING DATE: 2001-06-04
 ; PRIOR APPLICATION NUMBER: US 10/003,035
 ; PRIOR FILING DATE: 2001-11-01
 ; NUMBER OF SEQ ID NOS: 75
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 41
 ; LENGTH: 486
 ; TYPE: DNA
 ; ORGANISM: Human immunodeficiency virus type 1
 US-10-280-915-41

Query Match 100.0%; Score 90; DB 48; Length 486;
 Best Local Similarity 100.0%; Pred. No. 1.1e-17;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGAGGAAATAATCAGCACTTGAGATGGGGTGGAGATGGGGCACCATG 60
 Db 1 ATGAGATGAGGAAATAATCAGCACTTGAGATGGGGTGGAGATGGGGCACCATG 60

Qy 61 CTCCCTGGATGTGATGATCTGATGCT 90
 Db 61 CTCCCTGGATGTGATGATCTGATGCT 90

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; TELEFAX: 864-233-2284 ; SOFTWARE: PatentIn version 3.1
; INFORMATION FOR SEQ ID NO: 66: ; SEQ ID NO: 42
; SEQUENCE CHARACTERISTICS: ; LENGTH: 615
; LENGTH: 564 base pairs ; TYPE: DNA
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-628-686-66

Query Match 100.0%; Score 90; DB 10; Length 564;
Best Local Similarity 100.0%; Pred. No. 1.2e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
Organism: Human immunodeficiency virus type 1
US-10-003-035-42

Query Match 100.0%; Score 90; DB 43; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
Organism: Human immunodeficiency virus type 1
US-10-003-035-42

Qy 1 ATGAGACTGAAAGAGAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
Db 1 ATGAGACTGAAAGAGAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60

Qy 61 CTCCCTGGATGTGGATCTGTGAGATGGGGTGGAGATGGGCACCATG 90
Db 61 CTCCCTGGATGTGGATCTGTGAGATGGGGTGGAGATGGGCACCATG 90

Db 497 CTCCCTGGATGTGGATCTGTGAGATGGGGTGGAGATGGGCACCATG 526

RESULT 13
US-10-280-915-42
; Sequence 42, Application US/10280915
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: MULTIVALENT VACCINATION USING RECOMBINANT ADENOVIRUS
; FILE REFERENCE: 22488-741
; CURRENT APPLICATION NUMBER: US/10/280,915
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 42
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-280-915-42

Query Match 100.0%; Score 90; DB 48; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
Organism: Human immunodeficiency virus type 1
US-10-280-915-42

Qy 1 ATGAGACTGAAAGAGAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
Db 1 ATGAGACTGAAAGAGAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60

Db 61 CTCCCTGGATGTGGATCTGTGAGATGGGGTGGAGATGGGCACCATG 90
Db 61 CTCCCTGGATGTGGATCTGTGAGATGGGGTGGAGATGGGCACCATG 90

RESULT 14
US-10-286-332A-42
; Sequence 42, Application US/10286332A
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: METHOD OF VACCINATION THROUGH SEROTYPE ROTATION
; FILE REFERENCE: 22488-738
; CURRENT APPLICATION NUMBER: US/10/286,332A
; CURRENT FILING DATE: 2003-03-17
; PRIOR APPLICATION NUMBER: US 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
US-10-286-332A-42

Query Match 100.0%; Score 90; DB 1; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17; Indels 0; Gaps 0;
Matches 90; Conservative 0; Mismatches 0; Delins 0; Gaps 0;
Organism: Human immunodeficiency virus type 1
US-10-003-035-42

Qy 1 ATGAGACTGAAAGAGAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60
Db 1 ATGAGACTGAAAGAGAATATCAGCACTTGTGGAGATGGGGTGGAGATGGGCACCATG 60

Qy 61 CTCCCTGGATGTGGATCTGTGAGATGGGGTGGAGATGGGCACCATG 90
Db 61 CTCCCTGGATGTGGATCTGTGAGATGGGGTGGAGATGGGCACCATG 90

RESULT 15
US-10-003-035-42
; Sequence 42, Application US/10003035
; GENERAL INFORMATION:
; APPLICANT: Wang, Danher
; TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
; FILE REFERENCE: 22488-712
; CURRENT APPLICATION NUMBER: US/10/003,035
; CURRENT FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: 09/585,599
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US01/18238
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 10/003,035
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
US-10-003-035-42

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; SEQ ID NO 42
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Human immunodeficiency virus type 1
US-10-286-332A-42

Query Match 100.0%; Score 90; DB 48; Length 615;
Best Local Similarity 100.0%; Pred. No. 1.2e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGAGATGAAAGAAATACTAGCACTGTGGAGATGGGTGGAGATGGGCACCATG 60
Db      1 ATGAGATGAAAGAAATACTAGCACTGTGGAGATGGGTGGAGATGGGCACCATG 60
Qy      61 CTCCTGAGATGTGATGATCTAGTCT 90
Db      61 CTCCTGAGATGTGATGATCTAGTCT 90

RESULT 15
PCT-US02-35112-47
Sequence 47, Application PC/TU0235112
GENERAL INFORMATION:
APPLICANT: Wang, Danher
TITLE OF INVENTION: GENETIC VACCINE AGAINST HUMAN IMMUNODEFICIENCY VIRUS
FILE REFERENCE: 2248-740
CURRENT APPLICATION NUMBER: PCT/US02/35112
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: US 09/585,599
PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US01/18238
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: US 10/003,035
PRIOR FILING DATE: 2001-11-01
NUMBER OF SBQ ID NOS: 75
SOFTWARE: PatentIn version 3.1
SEQ ID NO 47
LENGTH: 786
TYPE: DNA
ORGANISM: Human immunodeficiency virus type 1
PCT-US02-35112-47

Query Match 100.0%; Score 90; DB 1; Length 786;
Best Local Similarity 100.0%; Pred. No. 1.3e-17;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy      1 ATGAGATGAAAGAAATACTAGCACTGTGGAGATGGGTGGAGATGGGCACCATG 60
Db      1 ATGAGATGAAAGAAATACTAGCACTGTGGAGATGGGTGGAGATGGGCACCATG 60
Qy      61 CTCCTGAGATGTGATGATCTAGTCT 90
Db      61 CTCCTGAGATGTGATGATCTAGTCT 90

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Search completed: March 12, 2004, 01:30:49
 Job time : 2284.3 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:52:43 ; Search time 562.569 seconds
 (without alignments)
 6934.037 Million cell updates/sec

Title: US-10-003-035-74
 Perfect score: 90
 Sequence: 1 atgaggatggaggaaata.....tgttgatgttgttgtgtc 90

Scoring table: IDENTITY_NUC

Gapop 10_0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

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2: gb_ng:*

3: gb_in:*

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10: gb_ro:*

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12: gb_sy:*

13: gb_un:*

14: gb_v1:*

15: em_ba:*

16: em_fun:*

17: em_num:*

18: em_in:*

19: em_mu:*

20: em_on:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_p1:*

26: em_to:*

27: em_sts:*

28: em_un:*

29: em_v1:*

30: em_htg_hum:*

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34: em_htg_pln:*

35: em_htg_rod:*

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37: em_htg_vrt:*

38: em_sy:*

39: em_ntgo_hum:*

40: em_ntgo_mus:*

41: em_ntgo_other:*

score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	90	100.0	105	I20806	I20806 Sequence 14
2	90	100.0	210	I08400	I08400 Sequence 1
3	90	100.0	430	I4_AF051948	AF051948 HIV-1 iso
4	90	100.0	430	I4_S77533	S77533 rev, vpu (H
5	90	100.0	470	I4_AF158148	AF158148 HIV-1 iso
6	90	100.0	1537	I4_AF21085	AF21085 Simian-Hu
7	90	100.0	1537	I4_AF201381	AF201381 Simian-Hu
8	90	100.0	2020	I4_AR360238	AR360238 Sequence
9	90	100.0	2028	I4_AR360240	AR360240 Sequence
10	90	100.0	2060	I4_AR360242	AR360242 Sequence
11	90	100.0	2552	I4_I05789	I05789 Sequence 8
12	90	100.0	2563	I4_AF189159	AF189159 HIV-1 iso
13	90	100.0	2568	I4_AY426110	AY426110 HIV-1 iso
14	90	100.0	2568	I4_AY426111	AY426111 HIV-1 clo
15	90	100.0	2568	I4_AY426112	AY426112 HIV-1 clo
16	90	100.0	2568	I4_AY426113	AY426113 HIV-1 clo
17	90	100.0	2568	I4_AY426114	AY426114 HIV-1 clo
18	90	100.0	2568	I4_AY426115	AY426115 HIV-1 clo
19	90	100.0	2568	I4_AY426116	AY426116 HIV-1 clo
20	90	100.0	2568	I4_AY426117	AY426117 HIV-1 clo
21	90	100.0	2568	I4_AY426118	AY426118 HIV-1 clo
22	90	100.0	2571	I4_AR05189	AR05189 Sequence
23	90	100.0	2571	I4_BD184664	BD184664 ANTI-CD4
24	90	100.0	2571	I4_AF358143	AF358143 HIV-1 clo
25	90	100.0	2571	I4_AF358145	AF358145 HIV-1 clo
26	90	100.0	2598	I4_I05783	I05783 Sequence 4
27	90	100.0	2691	I4_HIVU12030	HIVU12030
28	90	100.0	2692	I4_HIVU12031	HIVU12031
29	90	100.0	2694	I4_AR264703	AR264703 Sequence
30	90	100.0	2695	I4_AR097865	AR097865 Sequence
31	90	100.0	2730	I4_AR382220	AR382220 Sequence
32	90	100.0	2730	I4_AR365081	AR365081 Sequence
33	90	100.0	3084	I4_I83401	I83401 Sequence 2
34	90	100.0	3156	I4_E01088	E01088 Nucleic aci
35	90	100.0	3156	I4_M1410	M1410 Human immun
36	90	100.0	3563	I4_AR094671	AR094671 Sequence
37	90	100.0	3563	I4_AR382220	AR382220 Sequence
38	90	100.0	3563	I4_AR360189	AR360189 Sequence
39	90	100.0	3807	I4_U19867	U19867 Cloning vec
40	90	100.0	6031	I4_BD268910	BD268910 Anti-vira
41	90	100.0	8560	I4_AX03462	AX03462 Sequence
42	90	100.0	8560	I4_M15654	M15654 Human immun
43	90	100.0	8932	I4_AR094559	AR094559 Sequence
44	90	100.0	8933	I4_AR382018	AR382018 Sequence

ALIGNMENTS

RESULT 1	I20806	105 bp DNA	linear	PAT 07-OCT-1996
LOCUS	Sequence 14 from Patent US 5516657.			
DEFINITION				
ACCESSION	I20806			
VERSION	I20806.1			
KEYWORDS				
SOURCE	Unknown			
ORGANISM	Unclassified			
REFERENCE	1 (bases 1 to 105)			
AUTHORS	Murphy, C.I. and Young, B.			
TITLE	Baculovirus vectors for expression of secretory and membrane-bound			
PROTEINS	Proteins			
JOURNAL	PATENT, US 5516657-A, M, 14-MAY-1996,			

Pred. No. is the number of results predicted by chance to have a

FEATURES	source	Location/Qualifiers 1. .105 /organism="unknown" /mol_type="unassigned DNA"	AUTHORS Li,Q.-G., Zhang,Y.-J. and WadeLL,G. TITLE Direct Submission JOURNAL Submitted (02-MAR-1998) Virology, Umea University, Umea S-901 85, Sweden
ORIGIN			
Query Match	100.0%; Score 90; DB 6; Length 105; Best Local Similarity 100.0%; Pred. No. 2e-17; Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	FEATURES source 1. .430 /organism="Human immunodeficiency virus 1" /mol_type="genomic DNA" /isolate="BC9101" /db_xref="taxon:11676" /cell_line="Jurkat-tat III" /country="China" 93. .341 /gene="vpu" /pseudo 93. .341 /gene="vpu" /note="no start codon" /pseudo /codon_start=1	AUTHORS Li,Q.-G., Zhang,Y.-J. and WadeLL,G. TITLE Direct Submission JOURNAL Submitted (02-MAR-1998) Virology, Umea University, Umea S-901 85, Sweden
Db	1 ATGAGATGGAGAAATAATCAGCACTTGGAGATGGGGAGATGGGCCACCATG 60 10 ATGAGATGGAGAAATAATCAGCACTTGGAGATGGGGAGATGGGCCACCATG 69	gene	
Qy	61 CTCCCTGGATGGTTGATGACTGTGTTGCT 90	CDS	
Db	70 CTCCCTGGATGGTTGATGACTGTGTTGCT 99		
RESULT 2			
LOCUS	108400 210 bp DNA	LINEAR	PAT 02-DEC-1994
DEFINITION	Sequence 1 from Patent WO 8602930.		Query Match 100.0%; Score 90; DB 14; Best Local Similarity 100.0%; Pred. No. 2e-17; Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	108400		QY 1 ATGAGATGGAGAAATAATCAGCACTTGGAGATGGGGAGATGGGCCACCATG 60
VERSION	108400.1		Db 256 ATGAGATGGAGAAATAATCAGCACTTGGAGATGGGGAGATGGGCCACCATG 315
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 210) Essex,M.E. and Lee,T.-H.		
AUTHORS			
TITLE	ASSAY FOR DETECTING INFECTION BY HUMAN T-CELL LYMPHOTROPHIC VIRUS		
JOURNAL	Patent: WO 8602930-A 1 22-MAY-1986;		
FEATURES	Locations/Qualifiers 1. .210 /organism="unknown" /mol_type="unassigned DNA"		
ORIGIN	100.0%; Score 90; DB 6; Length 210;	RESULT 4 S77533 LOCUS	430 bp RNA linear VRL 06-MAY-2003 rev, vpu [human immunodeficiency virus type 1 HIV-1, BC9101, 430 nt].
Best Local Similarity 100.0%; Pred. No. 2e-17;		DEFINITION Chinese isolate, Genomic RNA Mutant, 430 nt.	
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		ACCESSION S77533 KEYWORDS	
Qy	1 ATGAGATGGAGAAATAATCAGCACTTGGAGATGGGGAGATGGGCCACCATG 60	SOURCE ORGANISM	Human immunodeficiency virus 1 (HIV-1) Human immunodeficiency virus 1 Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group
Db	1 ATGAGATGGAGAAATAATCAGCACTTGGAGATGGGGAGATGGGCCACCATG 60	REFERENCE AUTHORS	Li,Q.G., Zhang,Y.J., Liang,Y., Feng,C.Q., Li,Y.Z., Sjoberg,R., Jiang,Y., Wang,N.F. and WadeLL,G.
Qy	61 CTCCCTGGATGGTTGATGACTGTGTTGCT 90	TITLE	The morphogenesis of a Chinese strain of HIV-1 forming inclusion bodies in Jurkat-tat III cells
Db	61 CTCCCTGGATGGTTGATGACTGTGTTGCT 90	JOURNAL	J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 9 (2), 103-113 (1995)
RESULT 3			
LOCUS	AF051948 430 bp DNA linear VRL 17-MAR-1998	MEDLINE PUBMED	95268877 7749785
DEFINITION	HIV-1 isolate BC9101 from China, vpu pseudogene, complete sequence.	REMARK	GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 165679] from the original journal article. This sequence comes from Fig. 9.
ACCESSION	AF051948	FEATURES source	1. .430 /organism="genomic RNA" /mol_type="genomic RNA" /db_xref="taxon:11676" <1. .93 /gene="rev" 93. .341 /gene="vpu" /note="no start codon"
VERSION	AF051948.1		
KEYWORDS			
SOURCE	Human immunodeficiency virus 1 (HIV-1) Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate lentivirus group		
ORGANISM			
REFERENCE	1 (bases 1 to 430) Li,Q.G., Zhang,Y.J., Liang,Y., Feng,C.Q., Li,Y.Z., Sjoberg,R., Jiang,Y., Wang,N.F. and WadeLL,G.		
AUTHORS			
TITLE	The morphogenesis of a Chinese strain of HIV-1 forming inclusion bodies in Jurkat-tat III cells		
JOURNAL	J. Acquir. Immune Defic. Syndr. Hum. Retrovirol. 9 (2), 103-113 (1995)		
MEDLINE	95268877		
PUBMED	7749785		
REFERENCE	2 (bases 1 to 430)	Query Match 100.0%; Score 90; DB 14; Best Local Similarity 100.0%; Pred. No. 2e-17;	

with live-virus vaccine and challenged with pathogenic SHIVKU-1 AIDS Res. Hum. Retroviruses 16 (15), 1571-1580 (2000)

JOURNAL AIDS Res. Hum. Retroviruses

16(15), 1571-1580 (2000)

PUBLMED 20507321

REF ID 11054270

REFERENCE 2 (bases 1 to 1537)

AUTHORS Sipp, H.L., Kumar, A. and Narayan, O.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-1999) Microbiology, Molecular Genetics and

Immunology, University of Kansas Medical Center, 3901 Rainbow Blvd,

Kansas City, KS 66160, USA

FEATURES Location/Qualifiers

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EKRA"

ORIGIN

Query Match

100.0%

Score 90; DB 14; Length 1537;

Best Local Similarity 100.0%; Pred. No. 1.9e-17;

Matches 90; Conservative 0; Mismatches 0; Gaps 0;

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ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 1..9e-17;
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Qy 61 CTCCCTGGGATGTGATCTGTAGTGGT 90
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ORIGIN

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 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CTCCTGGGATGTGATCTGTAGTGGT 90
 Db 61 CTCCTGGGATGTGATCTGTAGTGGT 90

ORIGIN

RESULT 13
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 LOCUS HIV-1 isolate BaL from USA envelope glycoprotein (env) gene,
 DEFINITION complete cds.
 ACCESSION AY426110
 VERSION AY426110.1
 KEYWORDS
 SOURCE Human immunodeficiency virus 1 (HIV-1)
 ORGANISM Human immunodeficiency virus 1 (HIV-1)
 Viruses; Retroviridae; Lentivirus; Primate
 lentivirus group.
 1..(bases 1 to 2563)
 AUTHORS Chaiken,T.L., LaBranche,C.C., Zhang,W., Canziani,G., Robinson,J.,
 Chaiken,T.L., LaBranche,C.C., Zhang,W., Canziani,G., Robinson,J.,
 Hoxie,J.A., and Doms,R.W.
 TITLE Stable exposure of the coreceptor-binding site in a CD4-independent
 HIV-1 envelope protein
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (11), 6359-6364 (1999)
 MEDLINE 99272698
 PUBMED 10339592
 REFERENCE 2 (bases 1 to 2563)
 AUTHORS LeBranche,C.C., Hoffman,T.L., Romano,J., Haggarty,B.S.,
 Edwards,T.G., Matthews,T.J., Doms,R.W. and Hoxie,J.A.
 TITLE Determinants of CD4 independence for a human immunodeficiency virus
 type 1 variant map outside regions required for coreceptor
 specificity
 J. Virol. 73 (12), 10310-10319 (1999)
 JOURNAL 20027260
 MEDLINE 10559349
 PUBMED 3 (bases 1 to 2563)
 REFERENCE LaBranche,C.C., Hoffman,T.L., Romano,J., Haggarty,B.S.,
 Edwards,T.G., Matthews,T.J., Doms,R.W. and Hoxie,J.A.
 AUTHORS Direct Submission
 TITLE Submitted (23-SEP-1999) Surgery, Duke University, 117 SORF, LaSalle
 Street Extension, Durham, NC 27710, USA
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Page 6

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ORIGIN

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Search completed: March 11, 2004, 21:24:07
 Job time : 565.569 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:51:27 ; Search time 212.202 Seconds
(without alignments) Million cell updates/sec

Title: US-10-003-035-74
Perfect score: 90
Sequence: 1 atgagatgtaaaggagaata.....tgttgatgtatgttgtgt 90

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124039041 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Score	Query	Match	Length	DB	ID	Description	
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				27	90	100.0	Aan80948 HIV prote
				28	90	100.0	Aav09364 GMCSF/HIV
				29	90	100.0	Aav09364 Human imm
				30	90	100.0	Adbb87752 HIV-1 BH1
				31	90	100.0	Add66274 HIV E mode
				32	90	100.0	Art05127 HIV virus
				33	90	100.0	Av09365 HIV-1/CD4
				34	90	100.0	Aan60128 Sequence
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				36	90	100.0	Add66265 HIV clone
				37	90	100.0	Adbb87750 HIV-1 BH1
				38	90	100.0	Add66272 HIV Env
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				41	90	100.0	Av60252 Insert re
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				44	90	100.0	Adbb87783 HIV-1 mod
				45	90	100.0	Add66305 Modified

ALIGNMENTS

RESULT 1

ID	ADB87801 standard; DNA; 90 BP.
XX	
AC	ADB87801;
XX	
DT	04-DEC-2003 (first entry)
XX	
DE	gp120 signal peptide DNA fragment.
XX	
KW	adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoacide; cytotoxic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX	
OS	Human immunodeficiency virus 1.
XX	
PN	US2002155127-A1.
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PP	01-NOV-2001; 2001US-00003035.
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PR	04-JUN-2001; 2001WO-US018438.
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PA	(WANG/) WANG D.
XX	
PI	Wang D;
XX	
DR	WPI; 2003-182621/18.
XX	
New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C or E, or tumor antigens.	
XX	
PS	Claim 21; Page 81; 156pp; English.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	90	100.0	90	9	ADB87801	Adb87801 gp120 sig	Add6325 HIV gp120
2	90	100.0	90	9	ADD6325	Ad61319 pVDBS2p67	Adt15319 pVDBS2p67
3	90	100.0	105	2	AAT01088	Aat01088 Vlons-gp1	Aat01088 Vlons-gp1
4	90	100.0	119	2	AAT01088	Aan92594 Nucleotid	Aan92594 Nucleotid
5	90	100.0	210	1	AAN80949	Adbb8770 HIV-1 p17	Adbb8770 HIV-1 p17
6	90	100.0	486	9	ADB8770	Ad66292 HIV p17 s	Ad66292 HIV p17 s
7	90	100.0	486	9	ADD66292	Aaq87557 Human T c	Aaq87557 Human T c
8	90	100.0	564	2	AAQ87557	Aaq87557 Plasmid p	Aaq87557 Plasmid p
9	90	100.0	564	2	AAQ89755	Adb87764 HIV-1 p17	Adb87764 HIV-1 p17
10	90	100.0	615	9	ADB87764	Ad616286 HIV p17/2	Ad616286 HIV p17/2
11	90	100.0	615	9	ADD66293	Adb87771 HIV p17 m	Adb87771 HIV p17 m
12	90	100.0	786	9	ADB87776	Adb87776 HIV p17 p24	Adb87776 HIV p17 p24
13	90	100.0	786	9	ADD66298	Adb87777 HIV p24 s	Adb87777 HIV p24 s
14	90	100.0	915	9	ADB87777	Add66299 HIV p24	Add66299 HIV p24
15	90	100.0	915	9	ADD66299	Adb87764 HIV-1 p17	Adb87764 HIV-1 p17
16	90	100.0	1179	9	ADB87764	Adb87771 HIV p17	Adb87771 HIV p17
17	90	100.0	1179	9	ADD66286	Adb87771 HIV p17/2	Adb87771 HIV p17/2
18	90	100.0	1308	9	ADB87765	Adb87765 HIV p17	Adb87765 HIV p17
19	90	100.0	1308	9	ADD66287	Adb87774 HIV p17/2	Adb87774 HIV p17/2
20	90	100.0	1533	7	ACC0121	Acc0121 Nucleotid	Acc0121 Nucleotid
21	90	100.0	2020	2	AAT04707	Aat04707 ALVAC rec	Aat04707 ALVAC rec
22	90	100.0	2028	2	AAT04708	Aat04708 COPAK rec	Aat04708 COPAK rec
23	90	100.0	2060	2	AAT04709	Aat04709 COPAK rec	Aat04709 COPAK rec

This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antiparasitic, antiviral, antiparasitic, protozoacide, cytotoxic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against

CC The glycosylated proteins are produced at a much higher level than in previous systems. These vectors can be used to produce HIV-1 gp120, and other envelope proteins. (Updated on 25-MAR-2003 to correct PF field.)

XX Sequence 105 BP; 28 A; 14 C; 37 G; 26 T; 0 U; 0 Other;

SQ Query Match Score 90; DB 2; Length 105;

Best Local Similarity 100.0%; Pred. No. 8e-20;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ATGAGACTGAGGAAATACTAGCACTTGTGGAGATGGGGTGGAGATGGCACCATG 60

DB 10 ATGAGACTGAGGAAATACTAGCACTTGTGGAGATGGGGTGGAGATGGCACCATG 69

QY 61 CTCCCTGGGAGCTTGATGATCTGATCTGATGCT 90

DB 70 CTCCCTGGGATCTGATCTGATCTGATGCT 99

RESULT 4

AAT01088

ID AAT01088 standard; cDNA; 119 BP.

XX AC AAT01088;

XX DT 26-MAR-1996 (first entry)

XX DE V1Jns-gp160IIIB construct junction sequence.

XX KW Polynucleotide vaccine; genetic immunisation; coordinate expression;

KW HIV-1; AIDS; human immunodeficiency virus; antigen; immunogen;

KW vector; V1Jns; gp160; promoter; terminator; CMVintA-BGH; ds; ss;

XX OS Synthetic.

XX PN W09524485-A2.

XX PD 14-SEP-1995.

XX PF 03-MAR-1995; 95WO-US002633.

XX PR 07-MAR-1994; 94US-00207526.

XX PA (MERI) MERCK & CO INC.

XX PI Liu MA, Shiver JW, Perry HC;

XX XX WPI; 1995-328276/42.

XX New poly-cistronic expression construct - for producing antigens and

PT immuno-stimulatory gene products useful as vaccines against e.g. HIV,

PT hepatitis, etc.

XX Claim 23: Page 138; 178pp; English.

XX The HIV 1 strain IIIB gp160 gene was inserted into V1Jns, a vector contg.

CC a CMVintA-BGH terminator construct (AAT0112) that allows controlled

expression of heterologous genes. The sequences across the 5' junction of

CC CMVintA (cytomegalovirus promoter and intron A) and the HIV gene, and

CC across the 3' junction of the HIV gene and BGH (bovine growth hormone)

CC terminator are given in AAT01088-89. The vector allows large-scale prodn.

CC of polynucleotide vaccine in bacterial host cells

XX SQ Sequence 119 BP; 33 A; 16 C; 40 G; 30 T; 0 U; 0 Other;

XX Query Match Score 90; DB 2; Length 119;

Best Local Similarity 100.0%; Pred. No. 8.2e-20;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

AC ATGAGACTGAGGAAATACTAGCACTTGTGGAGATGGGGTGGAGATGGCACCATG 60

DB 1 ATGAGACTGAGGAAATACTAGCACTTGTGGAGATGGGGTGGAGATGGCACCATG 69

QY 13 ATGAGACTGAGGAAATACTAGCACTTGTGGAGATGGGGTGGAGATGGCACCATG 72

CC 61 CTCCCTGGGATTTGATGATCTGATGCT 90

CC 73 CTCCCTGGGATTTGATGATCTGATGCT 102

RESULT 5

AAN92594

ID AAN92594 standard; DNA; 210 BP.

XX AC AAN92594;

XX DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 28-JUN-1990 (First entry)

XX DE Nucleotide sequence for the amino terminal portion of the HTLV-III envelope region gp 160 and gp 120.

DE XX Glycoproteins gp 120 and gp 160; HTLV-III; HTLV-III antibodies;

KW XX immunoassay.

OS XX Human lymphotropic virus type III.

XX FH XX Key

FT FT CDS

FT FT misc_feature

FT FT mat_peptide

FT FT

08-FBB-1996	(first entry)
KW	Human immunodeficiency virus; asymmetric; hammerhead; ribozyme; helix I;
KW	helix II; helix III; loop 2; cleavage site; amplification; PCR; primer;
XX	motif; construct; pathogen; retrovirus infection; ss.
OS	Synthetic.
XX	
PH	Key primer_bind
FT	Location/Qualifiers
FT	/*tag= ^
FT	/note= "binds primer AR6B"
FT	complement(213..-231)
FT	/*tag= b
FT	/note= "binds primer XHOW"
XX	
PN	WO9510608-A1.
XX	
PD	20-APR-1995.
XX	
PF	15-OCT-1993 ; 93WO-EP002853 .
XX	
PR	15-OCT-1993 ; 93WO-EP002853 .
XX	
PA	(FORT-) FORT FOUND RES & TECHNOLOGY HELLAS.
PA	(DKFZ-) DKFZ DEUT KREBSFORSCHUNGSZENTRUM STIFTUNG.
PA	DR : 1995-161795/21.
PT	Asymmetric hammerhead ribozyme(s) and constructs - having high catalytic
PT	activity and improved specificity, for inactivating target RNA e.g. in
PT	unwanted endogenous genes or pathogens.
XX	
PS	Example 2: Fig 7; 72pp; English.
XX	A portion of the human T cell lymphotrophic virus type III sequence
CC	(HTLVIII) between bases 5819-6382. The region between bases 37-231 of
CC	this sequence (bases 5855-6050 of the HTLVIII sequence) was amplified
CC	using the primers AAQ87559-9. This amplified region (AAQ87561) was
CC	digested with EcoRI and XbaI and ligated with the plasmid PBS-UCU
CC	(AAQ87563), also digested with EcoRI and XbaI, to generate the asymmetric
CC	ribozyme construct p(alpha)-Rz195 (AAQ87565). The plasmid PBS-UCU is
CC	generated by modification of the Helix I box site of plasmid PBS-Rz120 by
CC	the oligonucleotide UCU (AAQ87562). This is an example of an asymmetric
CC	ribozyme construct generated to recognise and cleave after the sequence
CC	GUC in the target RNA. The construct encodes the asymmetric ribozyme
CC	alpha-Y-Rz195 (AAQ87567) which cleaves the HTLVIII RNA sequence AAQ87566.
CC	The asymmetric ribozymes generated by transcription of the constructs can
CC	be used in treatments to suppress endogenous genes or genes of pathogens
CC	or pathogenic RNA e.g. in viral or retroviral infections such as HIV
CC	infection
XX	
SQ	Sequence 564 BP; 198 A; 93 C; 141 G; 132 T; 0 U; 0 Other;
Query Match	Score 90; DB 2; Length 564;
Best Local Similarity	100.0% ; Pred. No. 1.2e-19;
Matches	90; Conservative 0; Mismatches 0;
Indels	0; Gaps 0;
XX	
Qy	1 ATGAGAGTGAAGGAGAAATATCAGCACTTGAGATGGGGACCATG 60
Db	437 ATGAGAGTGAAGGAGAAATATCAGCACTTGAGATGGGGACCATG 496
Qy	61 CTCCCTGGATGTGATGATCTGATGTGAT 90
Db	497 CTCCCTGGATGTGATGATCTGATGTGAT 526
RESULT 9	
AAQ89755	
ID AAQ89755	standard; DNA; 564 BP.
XX	
Db	437 ATGAGAGTGAAGGAGAAATATCAGCACTTGAGATGGGGACCATG 60
Qy	1 ATGAGAGTGAAGGAGAAATATCAGCACTTGAGATGGGGACCATG 90
Db	61 CTCCCTGGATGTGATGATCTGATGTGAT 526

RESULT 10
 ID ADB87771 standard; DNA; 615 BP.
 XX ADB87771;
 XX DT 04-DEC-2003 (first entry)
 DE HIV-1 p17 membrane form DNA SEQ ID 42.
 XX adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
 XX anti-parasitic; protozoicide; cytostatic; immunomodulatory; vaccine;
 XX pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
 XX Human immunodeficiency virus 1.
 OS Human immunodeficiency virus 1.
 PN US2002155127-A1.
 XX 24-OCT-2002.
 XX 01-NOV-2001; 2001US-000003035.
 PP 02-JUN-2000; 2000US-00585599.
 PR 04-JUN-2001; 2001WO-US018238.
 PR 01-NOV-2001; 2001US-00003035.
 XX (WANG/) WANG D.
 PA XX Wang D;
 PT XX Wang D;
 DR XX WPI; 2003-182621/18.
 DR XX P-PSDB; ADD66296.
 XX New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C or E, or tumor antigens.
 XX Claim 30; Fig 51A; 156pp; English.
 PS This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic, immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoa, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the invention.
 XX Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 90; DB 9; Length 615;
 Best Local Similarity 100.0%; Pred. No. 1.3e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 DB 61 CTCCTGGATGTGATGATCTGTGCT 90
 DB 61 CTCCCTGGATGTGATCTGTGCT 90
 QY 1 ATGAGACTGAAAGGAAATAATCAGCACTTGAGATGGGGTGGAGATGGGGACCATG 60
 DB 1 ATGAGACTGAAAGGAAATAATCAGCACTTGAGATGGGGTGGAGATGGGGACCATG 60
 QY 61 CTCCCTGGATGTGATCTGTGCT 90
 DB 61 CTCCCTGGATGTGATCTGTGCT 90
 RESULT 12
 ADB87776 standard; DNA; 786 BP.
 XX ADB87776;
 AC DT 04-DEC-2003 (first entry)
 DE HIV-1 p24 secreted form DNA SEQ ID 47.
 XX HIV antigen; infection; anti-HIV; virucide; antibacterial;
 KW antiparasitic; protozoicide; cytostatic; immunomodulatory; vaccine;

KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
 XX OS Human immunodeficiency virus 1.
 XX US2002155127-A1.
 PN 24-OCT-2002.
 XX 01-NOV-2001; 2001US-00003035.
 PD 02-JUN-2000; 2000US-00585599.
 PR 04-JUN-2001; 2001WO-US018238.
 XX 01-NOV-2001; 2001US-00003035.
 PA (WANG/) WANG D.
 XX (WANG/) WANG D.
 PA Wang D;
 PI Wang D;
 XX DR WPI; 2003-851718/79.
 DR P-PSDB; ADD66301.
 XX Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprising administering to the host a first and a second recombinant adenovirus.
 PT Example; SEQ ID NO 47; 185pp; English.
 PS The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is used for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
 XX SQ Sequence 786 BP; 280 A; 146 C; 198 G; 162 T; 0 U; 0 Other;
 CC Query Match Score 100.0%;
 CC Best Local Similarity 100.0%;
 CC Matches 90; Pred. No. 1.3e-19;
 CC Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC QY 1 ATGAGATGAAAGAGAAATACTGACATTGTGAGATGGGCTGACATG 60
 CC Db 1 ATGAGATGAAAGAGAAATACTGACATTGTGAGATGGGCTGACATG 60
 CC QY 61 CTCCCTGGATGGTGTGATCTGTAGACTGTGGAGATGGGGTGGATCTGTAGTCCT 90
 CC Db 61 CTCCCTGGATGGTGTGATCTGTAGACTGTGGAGATGGGGTGGATCTGTAGTCCT 90
 RESULT 14
 ADB87777 standard; DNA; 915 BP.
 XX ID ADB87777
 XX AC ADB87777;
 XX DT 04-DEC-2003 (first entry)
 XX HIV-1 p24 membrane form DNA SEQ ID 48.
 DE Human immunodeficiency virus 1.
 XX US2002155127-A1.
 KW adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
 KW antiparasitic; protozoide; cyroscopic; immunomodulatory; vaccine;
 KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
 OS HIV p24 (first entry)
 XX HIV p24 secreted form DNA.
 DE HIV p24 secreted form DNA.
 XX AC ADD66298
 XX 15-JAN-2004 (first entry)
 DE ADD66298 standard; DNA; 786 BP.
 XX AC ADD66298;
 XX DT 15-JAN-2004 (first entry)
 DE HIV p24 secreted form DNA.
 KW virucide; hepatotropic; RNA editing; CP gene; vaccine; immunity enhanced;
 KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
 KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
 KW HIV infection; ds; gene.
 XX Human immunodeficiency virus.

PA (WANG/) WANG D.
 XX Wang D;
 PT
 XX DR WPI: 2003-182621/18.
 XX New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor antigens.
 PS Claim 30: Page 63: 156pp; English.
 XX This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumor antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the invention.

SQ Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 9; Length 915;
 Best Local Similarity 100.0%; Pred. No. 1.4e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAGAGTGAAGGAGAAATATCAGGACTTGAGCTGTGGAGATGGGGTGGAGATGGGGACCCATG 60
 Db 1 ATGAGAGTGAAGGAGAAATATCAGGACTTGAGCTGTGGAGATGGGGTGGAGATGGGGACCCATG 60

SQ Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
 Query Match 100.0%; Score 90; DB 9; Length 915;
 Best Local Similarity 100.0%; Pred. No. 1.4e-19;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAGAGTGAAGGAGAAATATCAGGACTTGAGCTGTGGAGATGGGGTGGAGATGGGGACCCATG 60
 Db 1 ATGAGAGTGAAGGAGAAATATCAGGACTTGAGCTGTGGAGATGGGGACCCATG 60

Qy 61 CTCCCTGGGATGTTGATGATCTGTAGTGTCTG 90
 Db 61 CTCCCTGGGATGTTGATGATCTGTAGTGTCTG 90

Qy 61 CTCCTGGGATGTTGATGATCTGTAGTGTCTG 90
 Db 61 CTCCTGGGATGTTGATGATCTGTAGTGTCTG 90

SEARCH RESULTS

RESULT 15
 ADD66299
 ID ADD66299 standard; DNA; 915 BP.
 XX AC ADD66299;
 XX DT 15-JAN-2004 (first entry)
 XX DE HIV p24 membrane form DNA.
 XX KW viricide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
 KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
 KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
 KW HIV infection; ds; gene.
 XX OS Human immunodeficiency virus.
 PN US2003138459-A1.
 XX PD 24-JUL-2003.
 XX PF 17-MAR-2003; 2003US-00286332.
 XX PR 02-JUN-2000; 2000US-00585599.
 PR 04-JUN-2001; 2001WO-05018238.
 PR 01-NOV-2001; 2001US-00003035.
 XX PA (WANG/) WANG D.
 XX

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:51:27 ; Search time 254.642 Seconds

(without alignments) (1801.765 Million cell updates/sec)

Title: US-10-003-035-25

Perfect score: 108

Sequence: 1 tgatcaaaggcccaaaacaaa.....atatgagacaaggcacatgt 108

Scoring table: IDENTITY_NUC Gapop 10_0 , Gapext 1.0

Searched: 3373853 seqs, 2124093041 residues

Total number of hits satisfying chosen parameters:

6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002s:*

7: Geneseqn2003s:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

RESULT 1
 ADB87754

ID ADB87754 standard; DNA; 108 BP.

XX

AC ADB87754;

XX DT 04-DEC-2003 (first entry)

XX DR HIV-1 BH10 V3 loop clade B SEQ ID 25.

XX XX

adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoa; cytotoxic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds. KW KW KW KW KW KW KW KW KW

Human immunodeficiency virus 1.

OS OS

XX Human immunodeficiency virus 1.

XX PN US2002155127-A1.

XX PD 24-OCT-2002.

XX XX PP 01-NOV-2001; 2001US-00003035.

XX PR 02-JUN-2000; 2000US-0058599.

XX PR 04-JUN-2001; 2001WO-US01238.

XX PA (WANG /) WANG D.

XX PI Wang D;

XX DR WPI; 2003-182621/18.

XX New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C or E, or tumor antigens.

XX Claim 17; Fig 48; 156pp; English.

XX This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytotoxic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against

ALIGNMENTS

24	108	100.0	1920	1	AAN81452 Sequence
25	108	100.0	2280	9	ADB87745 HIV-1 str
26	108	100.0	2280	9	Add66267 HIV clone
27	108	100.0	2457	1	AAN81451 Sequence
28	108	100.0	2562	9	ADB87761 HIV-1 BH1
29	108	100.0	2562	9	Add66283 Modified
30	108	100.0	2583	9	ADB87753 HIV-1 BH1
31	108	100.0	2583	9	Add66275 HIV E m/E
32	108	100.0	2673	1	AAN81449 Sequence
33	108	100.0	2747	9	ADB87752 HIV-1 BH1
34	108	100.0	2747	9	Add66274 HIV E mde
35	108	100.0	2945	2	ART05127 HIV v-Trus
36	108	100.0	2950	9	ADB87757 HIV-1 BH1
37	108	100.0	2950	9	Add66273 HIV E mde
38	108	100.0	3157	9	ADB87743 HIV-1 str
39	108	100.0	3157	9	Add66265 HIV clone
40	108	100.0	3417	9	ADB87750 HIV-1 BH1
41	108	100.0	3417	9	Add66272 HIV Env_m
42	108	100.0	3839	9	ADB87781 HIV-1 mod
43	108	100.0	3839	9	Add66303 Modified
44	108	100.0	4040	9	ADB87783 HIV-1 mod
45	108	100.0	4040	9	Add66305 Modified

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	108	100.0	108	9	ADB87754	Adb87754 HIV-1 BH1
2	108	100.0	108	9	ADD66276	Add66276 Multi-clia
3	108	100.0	288	1	Aan90622	Sequence
4	108	100.0	288	2	AAQ04273	Sub 1, a
5	108	100.0	423	1	Aan90623	Sequence
6	108	100.0	423	2	AAQ04274	Sub 2, a
7	108	100.0	536	1	AAN92108	Aan92108 Synthetic
8	108	100.0	536	1	AAN90626	Aan90626 N-terminal
9	108	100.0	537	1	AAN90739	Aan90739 DNA encod
10	108	100.0	537	1	AAN90622	Aan90622 Polynucle
11	108	100.0	702	1	AAN81450	Aan81450 Sequence
12	108	100.0	702	1	AAN92112	Aan92112 Polynucle
13	108	100.0	702	2	AAQ35897	Aaq35897 Recombina
14	108	100.0	1056	1	AAN92109	Aan92109 Synthetic
15	108	100.0	1059	1	AAN90740	Aan90740 DNA encod
16	108	100.0	1059	1	Aan92117	Aan92117 Polynucle
17	108	100.0	1269	1	Aan90738	Aan90738 DNA encod
18	108	100.0	1269	1	Aan92115	Aan92115 Polynucle
19	108	100.0	1276	1	Aan92107	Aan92107 Synthetic
20	108	100.0	1533	7	ACC70121	Acc70121 Nucleotid
21	108	100.0	1791	1	Aan90741	Aan90741 DNA encod
22	108	100.0	1791	1	Aan92118	Aan92118 Sequence
23	108	100.0	1796	1	Aan92110	Aan92110 Synthetic

CC infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the invention.

XX Sequence 108 BP; 48 A; 18 C; 23 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCAGGACCCAAACAACTACAGAAGATCGGATTCAGAGGACGGGAGA 60
Db 1 TGTCAGGACCCAAACAACTACAGAAGATCGGATTCAGAGGACGGGAGA 60

XX Sequence 108 BP; 48 A; 18 C; 23 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 9; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.8e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCAGGACCCAAACAACTACAGAAGATCGGATTCAGAGGACGGGAGA 60
Db 1 TGTCAGGACCCAAACAACTACAGAAGATCGGATTCAGAGGACGGGAGA 60

RESULT 3
AAN90622
ID AAN90622 Standard; DNA; 288 BP.
XX
AC AAN90622;
XX
DE Sequence encoding Sub1 HIV fusion protein.
XX HIV; AIDS; Sub 1 fusion protein; HIV vaccine; ds.
XX
XX Simian-Human immunodeficiency virus.
OS
XX
FH Location/Qualifiers
Key
FT 91-.354
Misc_feature /*tag= a /label= HIV derived sequence
FT
XX
XX EP2306219-A.
PN
XX PD 08-MAR-1989.
XX PF 25-AUG-1988;
XX PR 27-AUG-1987;
XX PA (REPK) REPLIGEN CORP.
XX
PI Rusche JR, Putney SD, Jayaherian K, Farley J, Grimalia R, Lynn D;
PI Petro J, Okeeffe T;
XX DR WPI; 1989-070387/10.
DR P-PSDB; AAP34760.
XX
PT New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or
therapies of AIDS, esp. for prepn. of vaccines against HIV infection.
XX
PS Claim 1; Table 2; 29pp; English.
XX
CC Protein derivative stimulates a lymphocyte proliferative response in HIV-
infected humans, providing a means of diagnosis, protection and
therapeutic value. (Updated on 25-MAR-2003 to correct PR field.) (Updated
on 24-OCT-2003 to correct PA field.) (Updated on 24-OCT-2003 to
standardise OS field)
XX
SQ Sequence 288 BP; 106 A; 57 C; 67 G; 58 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 1; Length 288;
Best Local Similarity 100.0%; Pred. No. 9.2e-22;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTCAGGACCCAAACAACTACAGAAGATCGGATTCAGAGGACGGGAGA 60
Db 115 TGTCAGGACCCAAACAACTACAGAAGATCGGATTCAGAGGACGGGAGA 174

XX
PS Example; SEQ ID NO 25; 185pp; English.
XX
The invention relates to a method of enhancing the immunity of a host to
infection of a first and second pathogenic virus comprising administering
to the host a first and a second recombinant adenovirus. The method is
useful for enhancing immunity of the host to infections, e.g. influenza,
Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, or
simplex or human papilloma virus or HIV infections. The present sequence
is used in the exemplification of the invention.
XX Sequence 108 BP; 48 A; 18 C; 23 G; 19 T; 0 U; 0 Other;

Qy 61 GCATTGTACATAGAAGAAATAGGAAATAATGAGAACAGCACATGT 108

Db 175 GCATTGTTACAATAGGAAAATAGGAATATGAGACAGCACATGT 222

RESULT 4

AQ04273 standard; DNA; 288 BP.
 XX
 ID AAQ04273 ;
 AC AAQ04273 ;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-SEP-1990 (first entry)

XX Sub 1, a HIV fusion protein encoding sequence.

XX HIV; fusion protein; Sub 1; therapy; AIDS; principal neutralising domain;
 KW antibodies; diagnosis; prophylaxis; ss.
 XX Synthetic.

FH Key Location/Qualifiers
 FT CDS 1 288
 FT /tag= a
 FT /product= "HIV 10 kd fusion protein"
 FT /note= "Sub 1"
 FT 91..233
 FT /*tag= b
 FT /label= HIV portion of Sub 1

XX WO903984-A.
 XX
 PR 19-APR-1990.
 XX
 PF 03-OCT-1988; 88US-00252949.
 XX
 PR 03-OCT-1988; 88US-00252949.
 PR 01-JUN-1989; 89US-00359543.
 PR 19-SEP-1989; 89US-00407663.
 XX PA (REPK) REPLIGEN CORP.

XX Rusche JR, Putney SD, Jayaherian K, Farley J, Grimalia R, Lynn D,
 PI Lynn DU, Petrov J, Okeeffe T,
 XX WPI; 1989-070387/10.
 DR P-PSDB; AAP4801.

XX Rusche JR, Putney SD, Jayaherian K, Farley J, Grimalia R,
 PI Petrov J,
 XX WPI; 1990-147824/19.
 DR P-PSDB; AAR04492.

XX Principal neutralising domain of HIV variants - used for producing
 PT peptides(s) and antibodies for diagnosis, prophylaxis and/or therapy
 PT therapy of HIV infection.
 XX Disclosure; Page ?; 108PP; English.

XX The gene can be expressed in simian cells, and synthesis of HIV proteins
 CC can be detected immunologically. The recombinant protein product
 CC comprises a principal neutralising domain. The neutralising domain is
 CC bounded by cysteine residues which occur at positions 296 and 331, the
 CC segments of the residues form a loop. See also AAR04427-R04506 and
 CC AAQ04273-Q04279. (Updated on 25-MAR-2003 to correct PR field.) (Updated
 CC on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct
 CC PI field.)

XX Sequence 288 BP; 106 A; 57 C; 67 G; 58 T; 0 U; 0 Other;
 CC Query Match 100.0%; Score 108; DB 2; Length 288;

CC Best Local Similarity 100.0%; Pred. No. 9.2e-22;
 CC Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ 1 TGTACAAGACCCAAACAACTACAGAAAAGTATCCGATCCGAGAGCAGGGAGA 60
 CC 115 TGTACAAGACCCAAACAACTACAGAAAAGTATCCGATCCGAGAGCAGGGAGA 174
 CC QY 61 GCATTGTTACAATAGGAAAATAGGAATATGAGACAGCACATGT 108

Db 175 GCATTGTTACAATAGGAAAATAGGAATATGAGACAGCACATGT 222

Db 175 GCATTGTTACAATAGGAAAATAGGAATATGAGACAGCACATGT 222

RESULT 5

AAN90623 standard; DNA; 423 BP.
 XX
 ID AAN90623
 AC AAN90623 ;
 XX
 DT 24-OCT-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 22-JUN-1990 (first entry)

XX Sequence encoding Sub2 HIV fusion protein.

XX DE HIV; AIDS; Sub2 fusion protein; HIV vaccine; ds.
 XX OS Simian-Human immunodeficiency virus.
 XX FH Key Location/Qualifiers
 FT Misc_feature 91..408
 FT /*tag= a
 FT /label= HIV derived sequence

XX EP06219-A.
 XX PN EP06219-A.
 XX PD 08-MAR-1989.
 XX PP 25-AUG-1988; 88EP-00307889.
 XX PR 27-AUG-1987; 87US-00090080.

XX PA (REPK) REPLIGEN CORP.
 XX PI Rusche JR, Putney SD, Jayaherian K, Farley J, Grimalia R, Lynn D,
 PI Petrov J, Okeeffe T,
 XX WPI; 1989-070387/10.
 DR P-PSDB; AAP4801.

XX New HIV proteins and peptide(s) - used in diagnosis, prophylaxis or
 PT therapy of AIDS, esp. for prepn. of vaccines against HIV infection.
 XX CC Claim 1; Table 3; 29PP; English.

XX CC Proteins derivative stimulates a lymphocyte proliferative response in HIV-
 CC infected humans, providing a means of diagnosis, protection and
 CC therapeutic value. (Updated on 25-MAR-2003 to correct PR field.) (Updated
 CC on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to
 CC standardise OS field)

XX SQ Sequence 423 BP; 162 A; 74 C; 89 G; 98 T; 0 U; 0 Other;
 CC Query Match 100.0%; Score 108; DB 1; Length 423;

CC Best Local Similarity 100.0%; Pred. No. 9.7e-22;
 CC Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 TGTAACAGACCCAAACAACTACAGAAAAGTATCCGATCCGAGAGCAGGGAGA 60
 CC 115 TGTAACAGACCCAAACAACTACAGAAAAGTATCCGATCCGAGAGCAGGGAGA 174
 CC Db 175 GCATTGTTACAATAGGAAAATAGGAATATGAGACAGCACATGT 222

Db 175 GCATTGTTACAATAGGAAAATAGGAATATGAGACAGCACATGT 222

RESULT 6

AQ04274 standard; DNA; 423 BP.
 XX
 ID AQ04274
 AC AAQ04274 ;
 XX
 DT 25-MAR-2003 (revised)

QY 1 TGTACAAGACCCAAACAACTACAGAAAAGTATCCGATCCGAGAGCAGGGAGA 60
 CC 115 TGTAACAGACCCAAACAACTACAGAAAAGTATCCGATCCGAGAGCAGGGAGA 174
 CC QY 61 GCATTGTTACAATAGGAAAATAGGAATATGAGACAGCACATGT 108

DT	20-SEP-1990	(first entry)	DT	10-MAR-2003	(revised)
XX	Sub 2, a HIV fusion protein encoding sequence.		DT	02-MAR-1990	(first entry)
DE	HIV; fusion protein; Sub 2; therapy; AIDS; principal neutralising domain;		XX	Synthetic polynucleotide encoding HTLV-III gp120 envelope protein.	
KW	antibodies; diagnosis; prophylaxis; ss.		XX	HTLV-III envelope protein gp120; PPB1; PB1;	
XX	Synthetic.		XX	lymphocyte proliferative response; AIDS.	
OS			XX	Synthetic.	
XX			OS		
XX	Key	Location/Qualifiers	XX		
XX	CDS	1..423	XX		
FT			XX		
FT		/product= "HIV 18 kd fusion protein"	XX		
FT			XX		
FT	Region	91..407	XX		
FT			XX		
FT		/label= HIV portion of Sub 2	XX		
XX	PN	WO9003984-A.	XX		
XX	PD	19-APR-1990.	XX		
XX	PP	03-OCT-1988;	XX		
XX	PP	88US-00252949.	XX		
PR	03-OCT-1988;	88US-00252949.	XX		
PR	03-JUN-1989;	89US-0035543.	XX		
PR	19-SEP-1989;	89US-00407663.	XX		
XX	PA	(REPK) REPLIGEN CORP.	PS	Example 4: Table 5; 85pp; English.	
XX	PI	Rusche JR, Purney SD, Javaherian K, Farley J, Grimalia R;	CC	It is a synthetic fragment which encodes a portion of HTLV-III gp120 envelope protein. It has a blunt end on the 5' end and a CTAG overhang on the non-coding strand at the 3' end which will ligate with BamHI. Used in example to construct PPB1 which is used to express the recombinant HTLV-III fusion protein PB1. PB1 is used to stimulate lymphocyte proliferative response in HTLV-III infected humans. It is suggested that PB1 can be used in the diagnosis, prophylaxis or therapy of AIDS. (Updated on 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)	
XX	DR	WPI: 1990-14784/19.	XX		
XX	DR	P-PSDB; ARI0443.	XX		
XX	PS	Disclosure: Page ?; 108pp; English.	XX		
XX	CC	The gene can be expressed in simian cells, and synthesis of HIV proteins can be detected immunologically. The recombinant protein product comprises a principal neutralising domain. The neutralising domain is bounded by cysteine residues which occur at positions 296 and 331, the segments by the residues form a loop. See also AAR04427-R04506 and AAQ04273-Q04279. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct CC field.)	CC		
XX	PS	Sequence 423 BP; 162 A; 74 C; 89 G; 98 T; 0 U; 0 Other;	CC		
XX	Query Match	100.0%; Score 108; DB 2; Length 423;	CC		
CC	Best Local Similarity	100.0%; Pred. No. 9.7e-22;	CC		
CC	Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC			
CC			RESULT 8	AAN90626	
CC			XX	AAN90626 standard; DNA; 536 BP.	
Db	Qy	1 TGATCAGACCAACAACTACAGAAAGTATCGTATCCAGAGAACGGGA 60	AC	AAN90626;	
Db	Db	115 TGATCAGACCAACAACTACAGAAAGTATCGTATCCAGAGAACGGGA 174	XX		
Qy	Qy	61 GCATTCTGATACATAGGAAATAATGAGAAGCATGT 108	XX	24-OCT-2003 (revised)	
Db	Db	175 GCATTCTGATACATAGGAAATAATGAGAAGCATGT 222	XX	25-MAR-2003 (revised)	
XX	XX		XX	22-MAR-1990 (first entry)	
XX	XX		XX	N-terminal region of PB1.	
XX	XX		DE		
XX	XX		KW	HIV; AIDS; env gene; HIV vaccine; ds.	
XX	XX		OS	Simian-Human immunodeficiency virus.	
XX	XX		PN	EP306219-A.	
XX	XX		DT	25-MAR-2003 (revised)	
XX	XX		RESULT 7	AAN92108	
XX	XX		ID	AAN92108 standard; DNA; 536 BP.	
XX	XX		AC	AAN92108;	
XX	XX		XX	EP306219-A.	
XX	XX		DT	25-MAR-2003 (revised)	

PD	08-MAR-1989.		DR	P-BSDB; AAP93537.
XX			XX	Recombinant HIV proteins - used in assays for detecting and quantifying antibody against HIV and for incorporation into vaccine compns.
PF	25-AUG-1988;	88EP-00307889.	PT	
XX			PT	
PR	27-AUG-1987;	87US-00090080.	PT	
XX			PT	
PA	(REPK) REPLIGEN CORP.		XX	
XX	Rusche JR, Putney SD, Jayaherian K, Farley J, Grimalia R, Lynn D;	PI	XX	It is an example of a nucleotide sequence coding for a novel protein which is composed of the HIV portion of fusion protein PB1, with or without the N-terminal Met. The novel protein is claimed and so are transfer vectors comprising AAN90740, eg plasmids pdeltaPB1 and pd2PB1. PB1 is disclosed in EPA 0255190. The novel protein can be used in assays for detecting or quantifying anti-HIV antibody and may be incorporated into vaccine compositions. (Updated on 25-MAR-2003 to correct PA field.)
XX	DWI ; 1989-070387/10.	DR	XX	
XX	New HIV Proteins and peptide(s) - used in diagnosis, prophylaxis or therapy of AIDS, esp. for prepn. of vaccines against HIV infection.	PT	XX	
XX	Disclosure; Page ?; 29PP; English.	PS	XX	
XX	Protein derivative stimulates a lymphocyte proliferative response in HIV-infected humans, providing a means of diagnosis, protection and therapeutic value. Synthetic proteins AAP90278-83 are derived from this sequence. (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)	CC	XX	
XX	Sequence 536 BP; 218 A; 86 C; 106 G; 126 T; 0 U; 0 Other;	QY	1 TGTACAGACCCAAAGACATACTACAGAAAGATGTCAGGAGGACATTGT 108	
XX	Query Match Score 108%; Best Local Similarity 100.0%; Pred. No. 1e-21; Length 536; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	28 TGATCAGACCCAAAGACATACTACAGAAAGATGTCAGGAGGACATTGT 135	
XX	Sequence 536 BP; 218 A; 86 C; 106 G; 126 T; 0 U; 0 Other;	QY	61 GCATTTGTTACAATAGGAAAAATAGGAAATATGAGCAAGGACATTGT 108	
XX	Query Match Score 108%; Best Local Similarity 100.0%; Pred. No. 1e-21; Length 536; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	88 GCATTTGTTACAATAGGAAAAATAGGAAATATGAGCAAGGACATTGT 135	
XX	RESULT 9 AAN90739	DE	RESULT 10 AAN92116	
XX	ID AAN90739 standard; DNA; 537 BP.	DT	ID AAN92116 standard; DNA; 537 BP.	
XX	AAN90739;	AC	AC AAN92116;	
XX	DT 25-MAR-2003 (revised) DT 08-JUN-1990 (first entry)	XX	XX	
XX	DNA encoding HIV portion of fusion protein PB1.	XX	Human lymphotrophic virus typ.	
DE		XX	OS Chimeric.	
XX	HIV; pdeltaPB1; pd2PB1; transfer vector; immunosorbent;	XX	KW	
XX	KW vaccine. env gene; HTLV-III; fusion protein PB1.	XX	KW lymphocyte proliferative response; AIDS.	
XX	OS Human immunodeficiency virus.	XX	XX	
XX	Key Location/Qualifiers CDS 1 . 537 /*tag= a	PA	OS Human lymphotrophic virus typ.	
XX	FT PR	PA	DE	
XX	XX EP311228-A.	PA	DN WPI; 1989-157957/22.	
XX	XX PD 12-APR-1989.	DR	DR P-PSDB; AAP92014.	
XX	XX PF 25-MAR-1988;	XX	XX Recombinant human T-cell leukaemia virus 3 proteins - used for stimulating lymphocyte proliferative response and in diagnosis of AIDS.	
XX	XX PR 09-OCT-1987;	XX	XX Table 13A; Page ?; 85pp; English.	
XX	XX PA (REPK) REPLIGEN CORP.	XX	CC It encodes the HIV portion of HTLV-III fusion Protein PB1. PB1 is produced from plasmid pPB1 which contains the HTLV-III env gene from pBu II - Bgl II. The protein encoded by this polypeptide is used to stimulate lymphocyte proliferative response in HTLV-III infected humans.	
XX	XX PI Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;	XX	CC CC CC	

CC It is suggested that this protein can be used in the diagnosis, CC prophylaxis or therapy of AIDS and for the preparation of vaccines, CC against HTLV-III. (Updated on 10-MAR-2003 to add missing OS field.) CC (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to CC correct PA field.)

SQ Sequence 537 BP; 218 A; 86 C; 106 G; 127 T; 0 U; 0 Other;

Query Match 100.0%; Score 108; DB 1; Length 702;

Best Local Similarity 100.0%; Pred. No. 1..1e-21;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Sequence 100.0%; Score 108; DB 1; Length 537;

Best Local Similarity 100.0%; Pred. No. 1e-21;

Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX

Query Match 1 TGTACAGGCCAACACATAACAGAAAGATTCGGATCCAGAGGACAGGGAGA 60

DB 28 TGTACAGGCCAACACATAACAGAAAGATTCGGATCCAGAGGACAGGGAGA 87

QY 61 GCATTGTTACATAGGAAAATAGGAATATGAGAACATGT 108

DB 88 GCATTGTTACATAGGAAAATAGGAATATGAGAACATGT 135

RESULT 11

AAN81450 standard; DNA; 702 BP.

XX

AC AAN81450;

XX

DT 27-AUG-2003 (revised)

DT 25-MAR-2003 (revised)

DT 06-DBC-1990 (first entry)

XX

DE Sequence encoding fusion protein PB1 of HTLV-III envelope protein.

XX

KW Immunoassay; AIDS vaccine; antigen; immunogen; diagnostic; HIV; LAV; ds.

XX

OS Human T-cell lymphotropic virus type 3.

XX

KEY Location/Qualifiers

FT 1 .. .702

FT /*tag= a

XX

EP255190-A.

XX

PR 03-FEB-1988.

XX

PR 19-JAN-1987; 87PB-00300397.

XX

PR 01-AUG-1986; 86TS-00892680.

XX

(REPK) REPLIGEN CORP.

XX

PUTNEY SD, Lynn D, Javaherian K, Mueller WT, Farley J;

XX

WPI: 1988-030421/05.

DR P-PSDB; AAP81143.

XX

New fragments of HTLV-III envelope protein - useful in antibody detection

PT and vaccines, and new DNA coding sequences.

XX

Claim 12; Page 63; 84PP; English.

XX

Recombinant DNA transfer vectors which comprise all or part of the nucleotide sequence or equiv. contg. bases whose translated region codes for the R10, PB1, 590 or KH1 fragments of HTLV-III envelope protein. Host cells transformed with these vectors and HTLV-III envelope protein fragments R10, PB1, 590 and KH1 are claimed. These protein fragments are useful in immunoassays for detection of HTLV-III antibodies; as antigenic components of AIDS vaccines; also to stimulate lymphocyte proliferative response in infected individuals. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)

XX

Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;

DR P-PSDB; AAP81143.

XX

New fragments of HTLV-III envelope protein - useful in antibody detection

PT and vaccines, and new DNA coding sequences.

XX

Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;

CC	Query Match 100.0%; Score 108; DB 1; Length 702;
CC	Best Local Similarity 100.0%; Pred. No. 1..1e-21;
CC	Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX	
QY	1 TGTACAGGCCAACACATAACAGAAAGTATCGAGGACAGGGAGA 60
DB	115 TGTACAGGCCAACACATAACAGAAAGTATCGAGGACAGGGAGA 174
QY	61 GCATTGTTACATAGGAAAATAGGAATATGAGAACATGT 108
DB	175 GCATTGTTACATAGGAAAATAGGAATATGAGAACATGT 222
	RESULT 12
	AAN92112
ID	AAN92112 standard; DNA; 702 BP.
XX	
AC	AAN92112;
XX	
DT	25-MAR-2003 (revised)
DT	10-MAR-2003 (revised)
DT	02-MAR-1990 (first entry)
XX	
DE	Polynucleotide encoding HTLV-III fusion protein PB1.
XX	
KW	HTLV-III envelope gene; PB1; lymphocyte proliferative response;
KW	AIDS.
XX	
PB1	AU8821172-A.
XX	
PD	13-APR-1989.
XX	
PF	18-AUG-1988; 8BAU-00021172.
XX	
PR	09-OCT-1987; 87US-00107231.
XX	
PA	(REPK) REPLIGEN CORP.
XX	
PI	Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;
XX	
DR	WPI: 1989-157957/22.
DR	P-PSDB; AAP92010.
XX	
PT	Recombinant human T-cell leukaemia virus 3 proteins - used for
PT	stimulating lymphocyte proliferative response and in diagnosis
PT	of AIDS or therapy of AIDS.
PT	Table 9A; Page ?; 85pp; English.
PS	XX
PS	It encodes a protein called PB1 (25kDa) which is an HTLV fusion protein
CC	CC produced from PB1. PB1 contains the HTLV-III env gene from Pvu II - Bgl II. The HIV portion of PB1 is used to stimulate lymphocyte proliferative
CC	CC response in HTLV-III infected humans. It is suggested that the HIV
CC	CC portion can be used in the diagnosis, prophylaxis or therapy of AIDS and
CC	CC for the preparation of vaccines against HTLV-III. (Updated on 10-MAR-2003
CC	CC to add missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)
CC	(Updated on 25-MAR-2003 to correct PA field.)
XX	Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;
XX	
QY	1 TGTACAGGCCAACACATAACAGAAAGTATCGAGGACAGGGAGA 60
DB	115 TGTACAGGCCAACACATAACAGAAAGTATCGAGGACAGGGAGA 174

QY	61	GCAATTGGTACAAATAGGAAAATAATGAGACAGAACATTTG	108		DT	02-MAR-1990	(first entry)
Db	175	GCATTGGTACAAATAGGAAAATAATGAGACAGAACATTTG	222		XX		Synthetic polynucleotide encoding HTLV-III gp160 envelope protein.
RESULT 13							
AAQ35897					KW		HTLV-III envelope protein gp160; p590; 590;
ID AAQ35897					KW		Lymphocyte proliferative response; AIDS.
XX					XX		Synthetic.
AC AAQ35897;					OS		
XX					XX		
DT 25-MAR-2003					PN	AU821172-A.	
{revised}					XX		
DT 02-JUN-1993					PD	13-APR-1989.	
{first entry}					XX		
XX					PF	18-AUG-1988;	88AU-00021172.
DE Recombinant PBI fusion protein gene.					XX	09-OCT-1987;	87US-00107231.
XX					XX		
XX Human immunodeficiency virus; HIV; envelope protein; AIDS; ds.					PA	(REPK) REPLIGEN CORP.	
XX Synthetic.					XX		
OS					PI	Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;	
PN EPS525828-A2.					XX	WPI; 1989-157957/22.	
XX					XX		
PD 03-FEB-1993.					PT	Recombinant human T-cell leukaemia virus 3 proteins - used for	
XX					PT	stimulating lymphocyte proliferative response and in diagnosis	
PF 19-JAN-1987;					PT	of AIDS.	
XX					XX		
PR 01-AUG-1986;					PS	Example 6; Table 6; 85pp; English.	
XX					XX		
PA (REPK) REPLIGEN CORP.					CC	It is a synthetic fragment which encodes a portion of HTLV-III gp160 envelope protein. It has a blunt end on the 5' end and a TGA overhang on the non-coding strand at the 3' end which will ligate with HindIII. Used in example to construct pB90 which is used to express recombinant HTLV-III fusion protein 590. 590 is used to stimulate lymphocyte proliferative response in HTLV-III infected humans. It is suggested that 590 can be used in the diagnosis, prophylaxis or therapy of AIDS. (Updated on 10-MAR-2003 to add missing OS Field.) (Updated on 25-MAR-2003 to correct PF field.) (Updated on 25-MAR-2003 to correct PA field.)	
XX					CC		
PA (REPK) REPLIGEN CORP.					CC		
XX					CC		
PI Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J;					CC		
DR WPI; 1993-038178/05.					CC		
P-PSDB; AAR31943.					CC		
XX					CC		
PT New recombinant HIV envelope protein PB1 - for treatment, prevention and					CC		
XX					CC		
PT diagnosis of HIV and AIDS.					CC		
XX					CC		
PS Claim 4; Page 12; 18pp; English.					CC		
XX					CC		
CC The DNA sequence contains essentially the HIV env gene from the PvII site to BglII site and encodes a novel recombinant HIV envelope protein.					CC	Sequence 1056 BP; 384 A; 177 C; 255 G; 240 T; 0 U; 0 Other;	
CC This plasmid in a suitable host, E. coli, can be used to produce the					CC	Query Match 100.0%; Score 108; DB 1; Length 1056;	
CC HIV 26kD fusion protein PBI. The protein can be used in diagnosis (in					CC	Best Local Similarity 100.0%; Pred. No. 1..1e-21;	
CC immunochemical assays, as an immuno- adsorbant), prophylaxis (a vaccine)					CC	Mismatches 0; Indels 0; Gaps 0;	
CC or therapy of AIDS. Fragments of PBI can be used to stimulate a					CC	CC 1 TGTCACAGACCCAAACAACTACAGAAAGACTCGTATCAGAGGACCGGAGA 60	
CC lymphocyte proliferative response in HIV-infected humans. This would then					CC	25 TGTCACAGACCCAAACAACTACAGAAAGACTCGTATCAGAGGACCGGAGA 84	
CC stimulate the immune system to respond to HIV. (Updated on 25-MAR-2003 to					CC		
XX correct PN field.) (Updated on 25-MAR-2003 to correct PF field.)					CC		
XX Sequence 702 BP; 260 A; 129 C; 148 G; 165 T; 0 U; 0 Other;					CC	61 GCATTGTACATAGGAAAAATAATGAGAAATAATGAGAAAGCACATGT 108	
XX					CC	85 GCATTGTACATAGGAAAAATAATGAGAAATAATGAGAAAGCACATGT 132	
CC Query Match 100.0%; Score 108; DB 2; Length 702;					CC		
CC Best Local Similarity 100.0%; Pred. No. 1..1e-21;					CC		
CC Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					CC		
CC					CC		
QY 1 TGTCACAAGCCAAACAACTACAGAAAGACTCGTATCAGAGGACCGGAGA 60					RESULT 15	AAN90740 standard; DNA; 1059 BP.	
Db 115 TGTCACAAGCCAAACAACTACAGAAAGACTCGTATCAGAGGACCGGAGA 174					ID	AAN90740	
XX					XX		
QY 61 GCATTGTACATAGGAAAAATAATGAGAAATAATGAGAAAGCACATGT 108					AC	AAN90740;	
Db 175 GCATTGTACATAGGAAAAATAATGAGAAAGCACATGT 222					XX		
XX					DT	25-MAR-2003 (revised)	
AC AAN92109;					XX	08-JUN-1990 (first entry)	
XX					DE	encoding HIV portion of fusion protein 590.	
DT 25-MAR-2003 (revised)					XX	HIV; p590; pdeltapB1; pdpB1; transfer vector; immunoabsorbent;	
ID AAN92109 standard; DNA; 1056 BP.					XX	vaccine; env gene; HTLV-III; fusion protein 590.	
XX					OS	Human immunodeficiency virus.	
AC AAN92109;					XX	Location/Qualifiers	
XX					PF	1..1059	
DT 25-MAR-2003 (revised)					FT	/tag= a	
ID AAN92109					CDS		

XX EP311228-A.
 XX
 PN 12-APR-1989.
 XX PD 12-APR-1989.
 XX PR 25-MAR-1988; 88EP-00302695.
 XX PR 09-OCT-1987; 87US-00107703.
 XX PA (REPK) REPLIGEN CORP.
 PI Putney SD, Lynn D, Javaherian K, Mueller WT, Farley J,
 XX DR WPI; 1989-108200/15.
 DR P-PDB; AAP93538.
 XX PT Recombinant HIV proteins - used in assays for detecting and quantifying
 PT antibody against HIV and for incorporation into vaccine compsns.
 XX PS Fig 3; Page ?; 17pp; English.
 XX SQ It is an example of a nucleotide sequence coding for a novel protein.
 CC which is composed of the HIV portion of fusion protein 590, with or
 CC without the N-terminal Met. The novel protein is claimed and so are
 CC transfer vectors comprising AN9074, eg plasmids pdeltaP1 and pdPB1.
 CC 590 is disclosed in EPA 0255190. The novel protein can be used in assays
 CC for detecting or quantifying anti-HIV antibody and may be incorporated
 CC into vaccine compositions. (Updated on 25-MAR-2003 to correct PA field.)
 XX SQ Sequence 1059 BP; 384 A; 180 C; 255 G; 240 T; 0 U; 0 Other;
 Query Match 100.0%; Score 108; DB 1; Length 1059;
 Best Local Similarity 100.0%; Pred. No. 1..e-21;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TGTAACAGACCCAAACACATACTACAGAAAATGGAAATATGAGAACGACATTGT 108
 Db 28 TGTAACAGACCCAAACACATACTACAGAAAATGGAAATATGAGAACGACATTGT 108
 Qy 61 GCATTGTTACAATGGAAAATGGAAATATGAGAACGACATTGT 108
 Db 88 GCATTGTTACAATGGAAAATGGAAATATGAGAACGACATTGT 135

Search completed: March 11, 2004, 20:49:38
 Job time : 259.642 secs

GenCore version 5.1.6									
Copyright (c) 1993 - 2004 Compugen Ltd.									
Allelic search - nucleic search, using sw model									
March 11, 2004, 20:30:23 : Search time 54.4954 Seconds (without alignments) 1099.812 Million cell updates/sec									
US-10-003-035-25									
Sequit score:	108	tgtacaagacccaacaaacaa.....atatgagacaaggacatgt	108						
Sequit table:	IDENTITY_NUC								
Gapext 1.0	Gapext 1.0								
682109 seqs, 27475446 residues									
number of hits satisfying chosen parameters: 1365418									
DB seq length: 0									
DB seq length: 2000000000									
Processing: Minimum Match 0%									
Maximum Match 100%									
Listing First 45 summaries									
Sequence :									
Issued Patents NA: *									
1: /cgn2_6/picodata/2/in4/5A_COMBO.Seq.*									
2: /cgn2_6/picodata/2/in4/5B_COMBO.Seq.*									
3: /cgn2_6/picodata/2/in4/6A_COMBO.Seq.*									
4: /cgn2_6/picodata/2/in4/6B_COMBO.Seq.*									
5: /cgn2_6/picodata/2/in4/PCTUS_COMBO.Seq.*									
6: /cgn2_6/picodata/2/in4/backfile1.Seq.*									
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
%									
Score Query Match Length DB ID Description									
108	100.0	2945	6	5462872-1		Patent No. 5462872			
108	100.0	8932	3	US-09-124-900-1		Sequence 1, Appli			
108	100.0	8933	3	US-08-463-210-4		Sequence 4, Appli			
108	100.0	8933	3	US-09-620-958A-3		Sequence 3, Appli			
108	100.0	8933	3	US-09-620-958A-4		Sequence 4, Appli			
108	100.0	8933	4	US-08-463-028-4		Sequence 9, Appli			
108	100.0	8933	4	US-08-463-028-4		Sequence 4, Appli			
106.4	98.5	781	2	US-08-059-818-18		Sequence 18, Appli			
106.4	98.5	781	2	US-08-089-666-18		Sequence 18, Appli			
106.4	98.5	781	2	US-08-465-018-18		Sequence 18, Appli			
106.4	98.5	781	2	US-08-725-776-18		Sequence 18, Appli			
106.4	98.5	1497	2	US-08-488-022-18		Sequence 3 , Appli			
106.4	98.5	1568	1	US-08-446-017-18		Sequence 7, Appli			
106.4	98.5	1568	1	US-08-446-017-18		Sequence 7, Appli			
106.4	98.5	1568	1	US-08-289-459A-7		Sequence 7, Appli			
106.4	98.5	1568	1	US-08-387-867A-7		Sequence 7, Appli			
106.4	98.5	1571	2	US-08-037-816A-25		Sequence 25, Appli			
106.4	98.5	1571	2	US-08-530-146-25		Sequence 25, Appli			
106.4	98.5	2531	3	US-07-556-483-18		Sequence 18, Appli			
106.4	98.5	2571	2	US-07-916-088A-1		Sequence 1, Appli			
106.4	98.5	2644	3	US-08-472-240A-9		Sequence 9, Appli			
106.4	98.5	2694	1	US-08-147-850-01		Sequence 1, Appli			
106.4	98.5	3084	1	US-08-147-850-02		Sequence 2, Appli			
106.4	98.5	3125	2	US-08-037-816A-13		Sequence 13, Appli			
106.4	98.5	3125	2	US-08-188-563-15		Sequence 5, Appli			
106.4	9709	2				RESULT 2			
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FILE REFERENCE: 1939-112P
 CURRENT APPLICATION NUMBER: US/09/124,900
 PRIOR APPLICATION NUMBER: 1998-07-30
 PRIORITY FILING DATE: 1998-07-30
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 1
 LENGTH: 8932
 TYPE: DNA
 ORGANISM: Human immunodeficiency virus type 1
 US-09-124-900-1

Query Match 100.0%; Score 108; DB 3; Length 8932;
 Best Local Similarity 100.0%; Pred. No. 2.5e-24;
 Matches 108; Conservative 0; Nmbratches 0; Indels 0; Gaps 0;

Qy 1 TGTACAGACCAACAAACATAACAGAAAAAGTATCCGATCCAGAGGGAGA 60
 Db 6465 TGTACAGACCAACAAACATAACAGAAAAAGTATCCGATCCAGAGGGAGA 6524

Qy 61 GCATTGTACAATGGAAATAATGAAATATGACAGGCACATGT 108
 Db 6525 GCATTGTACAATGGAAATAATGAAATATGAGAACAGCACATGT 6573

RESULT 3
 US-08-463-210-4
 Sequence 4, Application US/08463210
 Patent No. 6001977
 GENERAL INFORMATION:
 APPLICANT: CHANG, Nancy T.
 APPLICANT: GALLO, Robert C.
 APPLICANT: WONG-STFAAL, Flossie
 TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Finnegan, L.L.P.
 STREET: 345 Park Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10154-0053

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,210
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/693, 866
 FILING DATE: 23-JAN-1985
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/659, 339
 FILING DATE: 10-OCT-1984
 ATTORNEY/AGENT INFORMATION:
 NAME: Serunian, Leslie A.
 REGISTRATION NUMBER: 35,353
 REFERENCE/DOCKET NUMBER: 2026-4193US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8933 base pairs
 TYPE: nucleic acid
 STRANDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO

ORIGINAL SOURCE:
 ORGANISM: HTLV-III
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..8933
 OTHER INFORMATION: /standard_name= "Clone BH10"
 OTHER INFORMATION: /note= "Corresponds to nucleotide positions 222 to 9154 in figure 3 of EP 8530760"
 OTHER INFORMATION: 9154 in figure 3 of EP 8530760"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 113..1648
 OTHER INFORMATION: /product= "gag"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 1408..4424
 OTHER INFORMATION: /product= "pol"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 4367..4975
 OTHER INFORMATION: /product= "sor"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 5560..8148
 OTHER INFORMATION: /product= "env"

US-08-463-210-4

Query Match 100.0%; Score 108; DB 3; Length 8933;
 Best Local Similarity 100.0%; Pred. No. 2.5e-24;
 Matches 108; Conservative 0; Nmbratches 0; Indels 0; Gaps 0;

Qy 1 TGPACAGACCCACAAACATAACAGAAAAAGTATCCAGAGGGACGGAGA 60
 Db 6466 TGPACAGACCCACAAACATAACAGAAAAAGTATCCAGAGGGACGGAGA 6525

Qy 61 GCATTGTACAATGGAAAATAGGAAATATGAGAACAGCACATGT 108
 Db 6526 GCATTGTACAATGGAAAATAGGAAATATGAGAACAGCACATGT 6573

RESULT 4
 US-09-620-958A-3
 Sequence 3, Application US/09620958A
 Patent No. 6294338
 GENERAL INFORMATION:
 APPLICANT: Numomura, Kiyotada
 TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
 FILE REFERENCE: GP-04-02-UT
 CURRENT APPLICATION NUMBER: US/09/620,958A
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 3
 LENGTH: 8933
 TYPE: RNA
 ORGANISM: Human Immunodeficiency Virus
 FEATURE:
 NAME/KEY: source
 LOCATION: (1)..(8933)
 OTHER INFORMATION: Sequence of transcripts produced from the BH10
 Patent No. 6294338
 OTHER INFORMATION: Plasmid.
 US-09-620-958A-3

Query Match 100.0%; Score 108; DB 3; Length 8933;
 Best Local Similarity 82.4%; Pred. No. 2.5e-24;
 Matches 89; Conservative 19; Nmbratches 0; Indels 0; Gaps 0;

Qy 1 TGPACAGACCCACAAACATAACAGAAAAAGTATCCAGAGGGACGGAGA 60
 Db 6466 TGPACAGACCCACAAACATAACAGAAAAAGTATCCAGAGGGACGGAGA 6525

Qy 61 GCATTGTACAATGGAAAATAGGAAATATGAGAACAGCACATGT 108
 Db 6526 GCATTGTACAATGGAAAATAGGAAATATGAGAACAGCACATGT 6573

Db 6526 GCAUUCGUACAUAGGAAAUAGGAUAUGAGACAAGGACAUUUGU 6573

RESULT 5

Sequence 4, Application US/09620958A

Patent No. 6294338

GENERAL INFORMATION:

APPLICANT: Numomura, Kiyotada

TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD

FILE REFERENCE: GP104-02-UT

CURRENT APPLICATION NUMBER: US/09/620,958A

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 4

TYPE: RNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: Sequence of the IAC-Asrc pseudo target

FEATURE:

Patent No. 6294338

NAME/KEY: mutation

LOCATION: (4135) .. (4155)

OTHER INFORMATION: Mutated positions: 4135, 4140-1, 4145, 4150, 4152-3, 4155

US-09-620-958A-4

Query Match Similarity 100.0%; Score 108; DB 3; Length 8933;

Best Local Similarity 82.4%; Pred. No. 2.5e-24;

Matches 89; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTACAGACCCAAACACATAAACAGAAATATCGTATCCGAGGAGCAGGGAGA 60

Db 6466 UGUACANGAGCCAAACACATAAACAGAAUAGUAUCCGUAUCCGAGGAGCAGGGAGA 6525

Qy 61 GCATTGTACATATGGAATAATAGGAATAATGAGAACAGCATGT 108

Db 6526 GCAUUCGUACAUAGGAAAUAGGAUAUAGAGACAAGGACAUUUGU 6573

RESULT 6

US-09-620-958A-9

Sequence 9, Application US/09620958A

Patent No. 6294338

GENERAL INFORMATION:

APPLICANT: Numomura, Kiyotada

TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD

FILE REFERENCE: GP104-02-UT

CURRENT APPLICATION NUMBER: US/09/620,958A

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 9

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 9

TYPE: RNA

ORGANISM: Artificial Sequence

OTHER INFORMATION: Sequence of the IAC-Bscr pseudo target

Patent No. 6294338

NAME/KEY: mutation

LOCATION: (4140) .. (4159)

OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152, 4156-57, 4159

US-09-620-958A-9

Query Match Similarity 100.0%; Score 108; DB 3; Length 8933;

Best Local Similarity 82.4%; Pred. No. 2.5e-24;

Matches 89; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTACAGACCCAAACACATAAACAGAAATATCGTATCCGAGGAGCAGGGAGA 60

Db 6466 UGUACAGACCCAAACACATAAACAGAAUAGUAUCCGUAUCCGAGGAGCAGGGAGA 6525

RESULT 7

US-08-463-028-4

Sequence 4, Application US/08463028

Patent No. 6610476

GENERAL INFORMATION:

APPLICANT: CHENG, Nancy T.

APPLICANT: GALLO, Robert C.

APPLICANT: WONG-STALI, Flossie

TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,028

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/693,866

FILING DATE: 23-JAN-1985

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/659,339

FILING DATE: 10-OCT-1984

ATTORNEY/AGENT INFORMATION:

NAME: Serunian, Leslie A.

REGISTRATION NUMBER: 35,353

REFERENCE/DOCKET NUMBER: 2026-4193US3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 751-6849

TELEFAX: (212) 751-6849

SEQUENCE CHARACTERISTICS:

LENGTH: 8933 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: HTLV-III

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..8933

OTHER INFORMATION: /standard_name= "Clone BH10"

Patent No. 6294338

NAME/KEY: mutation

LOCATION: (4140) .. (4159)

OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152, 4156-57, 4159

US-09-620-958A-9

Query Match Similarity 100.0%; Score 108; DB 3; Length 8933;

Best Local Similarity 82.4%; Pred. No. 2.5e-24;

Matches 89; Conservative 19; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTACAGACCCAAACACATAAACAGAAATATCGTATCCGAGGAGCAGGGAGA 60

Db 6466 UGUACAGACCCAAACACATAAACAGAAUAGUAUCCGUAUCCGAGGAGCAGGGAGA 6525

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 113..1648

OTHER INFORMATION: /product= "gag"

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 1408..4452

OTHER INFORMATION: /product= "pol1"

FEATURE:

NAME/KEY: mat_peptide

LOCATION: 4367..4975

OTHER INFORMATION: /product= "sor"

FEATURE:
i NAME/KEY: mat_peptide
i LOCATION: 5560_R148
i OTHER INFORMATION: /product= "env"

RESULT 9
US-08-463-028-4

Query Match 100.0%; Score 108; DB 4; Length 8933;
Best Local Similarity 100.0%; Pred. No. 2.5e-24;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGTACAGACCCAAACAAATACAGAAAGTATCGPATCCAGAGGACGGAGA 60
Db 6466 TGTACAGACCCAAACAAATACAGAAAGTATCGPATCCAGAGGACGGAGA 6525

Qy 61 GCATTGTACATAATAGGAAAATATGAGACAAAGCACATTGT 108
Db 6526 GCATTGTACATAATAGGAAAATATGAGACAAAGCACATGT 6573

RESULT 8
US-08-459-818-18

Sequence 18, Application US/08459818
Patent No. 5,885,795

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William A.
APPLICANT: Kiener, Peter A.

TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 781 base pairs
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US02
TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 781 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-08-889-666-18

Query Match 98.5%; Score 106.4; DB 2; Length 781;
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 10
US-08-465-078-18

Sequence 18, Application US/08465078
Patent No. 5,885,796

GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William A.
APPLICANT: Kiener, Peter A.

Qy 1 TGTACAGACCCAAACAAATACAGAAAGTATCGPATCCAGAGGACGGAGA 60
Db 563 TGTACAGACCCAAACAAATACAGAAAGTATCGPATCCAGAGGACGGAGA 622

Qy 61 GCATTGTACATAATAGGAAAATATGAGACAAAGCACATGT 108
Db 623 GCATTGTACATAATAGGAAAATATGAGACAAAGCACATGT 670

Query Match 98.5%; Score 106.4; DB 2; Length 781;
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/465,078

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/375390

FILING DATE: 18-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Adriano, Sarah B.

REGISTRATION NUMBER: 34,470

TELECOMMUNICATION INFORMATION:

TELEPHONE: 310-445-1140

TELEFAX: 310-445-9031

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 781 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-465-078-18

Query Match 98.5%; Score 106.4; DB 2; Length 781;
Best Local Similarity 99.1%; Pred. No. 4.2e-24;
Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Sequence for SEQ ID NO: 18:

Qy 1 TGTACAGACCCACAACATAAGAAATGATCCCTATCCAGAGGACCGGGAGA 60
Db 563 TGTACAGACCCACAACATAAGAAATGATCCCTATCCAGAGGACCGGGAGA 622

Qy 61 GCATTGTACATAGGAAAAATAGGAAATATGAGAAAGCACATTG 108
Db 623 GCATTGTACATAGGAAAATAGGAAATATGAGAAAGCACATTG 670

RESULT 12
US-08-468-062-18

Sequence 18, Application US/08488062
Patent No. 5977318
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
ATTORNEY: Ledbetter, Jeffrey A.
DAMILE, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould

STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,062
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390

REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
TELECOMMUNICATION INFORMATION:

NAME: Adriano, Sarah B.

TELEPHONE: 18-JAN-1995

TELEFAX: 310-445-9031

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 781 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-468-062-18

Sequence 18, Application US/08725776
Patent No. 5965150
GENERAL INFORMATION:
APPLICANT: Linsley, Peter S.
ATTORNEY: Ledbetter, Jeffrey A.
DAMILE, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Blvd., Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

TELEPHONE: 310-445-1140
 TELEFAX: 310-445-9031
 SEQUENCE CHARACTERISTICS:
 LENGTH: 781 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-488-062-18

Query Match 98.5%; Score 106.4; DB 2; Length 781;
 Best Local Similarity 99.1%; Pred. No. 4.2e-24;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGTACAAGACCAACACATACAGAAAGATCCGATCCGAGGACCGGGA 60
 Db 563 TGTACAAGACCAACACATACAGAAAGATCCGATCCGAGGACCGGGA 622
 Qy 61 GCATTGTGTACATAAGAAATAATGAGAACATGAGCACATTTG 108
 Db 623 GCATTGTGTACATAAGAAATAATGAGAACATGAGCACATTTG 670

RESULT 13
 US-07-916-09A-3
 Sequence 3, Application US/07916098A
 Parent No. 5871732

GENERAL INFORMATION:
 APPLICANT: BURKLY, LINDA C.
 APPLICANT: CHISHOLM, PATRICIA L.
 APPLICANT: THOMAS, DAVID W.
 APPLICANT: ROSA, MARGARET D.
 APPLICANT: ROSA, JOSEPH J.
 TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 TREATMENT OF AIDS, ARC AND HIV INFECTION
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
 STREET: 10 SOUTH WACKER DRIVE
 CITY: CHICAGO
 STATE: ILLINOIS
 COUNTRY: U.S.A.
 ZIP: 60606

COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/916,098A
 FILING DATE: JULY 24, 1992
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/08843
 FILING DATE: NO. 5871732ember 27, 1991
 CLASSIFICATION: 424
 APPLICATION NUMBER: 07/618,542
 FILING DATE: NO. 5871732ember 27, 1990
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: JOHN J MC DONNELL
 REGISTRATION NUMBER: 26,949
 REFERENCE/DOCKET NUMBER: 92,310-G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 715-1100
 TELEX: 910/221-5317
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1497 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1494
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1
 OTHER INFORMATION: /note= "soluble HIV gp120"
 US-07-916-09A-3

Query Match 98.5%; Score 106.4; DB 2; Length 1497;
 Best Local Similarity 99.1%; Pred. No. 5e-24;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGTACAAGACCCAAACAAATACTAGAAAGATCCGATCCGAGGACCGGGA 60
 Db 874 TGTACAAGACCCAAACAAATACTAGAAAGATCCGATCCGAGGACCGGGA 933
 Qy 61 GCATTGTGTACATAAGAAATAATGAGAACATGAGCACATTTG 108
 Db 934 GCATTGTGTACATAAGAAATAATGAGAACATGAGCACATTTG 981

RESULT 14
 US-08-589-446-7
 Sequence 7, Application US/08589446
 Patent No. 5614413

GENERAL INFORMATION:
 APPLICANT: Morrow, Casey D.
 APPLICANT: Morrow, Case D.
 TITLE OF INVENTION: ENCAPSULATED POLIOVIRUS NUCLEIC
 ACID AND METHODS OF MAKING AND
 TREATMENT OF INFECTION: USING SAME
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LAHIVE & COCKFIELD
 STREET: 60 STATE STREET, SUITE 510
 CITY: BOSTON
 STATE: MASSACHUSETTS
 COUNTRY: USA
 ZIP: 02109

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ASCII
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/589,446
 FILING DATE:
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US/08/087,009
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Geary III, William C.
 REGISTRATION NUMBER: 31,359
 REFERENCE/DOCKET NUMBER: UAG-004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7400
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1568 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 7..1565
 US-08-589-446-7

Query Match 98.5%; Score 106.4; DB 1; Length 1568;
 Best Local Similarity 99.1%; Pred. No. 5.1e-24;
 Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Job time : 59.4954 secs

Search completed: March 11, 2004, 23:12:13

QY 1 TGTACAAGCCAAACATAACAGAAAAAGTATCCGATCCAGAGGACAGGGAGA 60
 Db 280 TGTACAAGCCAAACATAACAGAAAAAGTATCCGATCCAGAGGACAGGGAGA 339

QY 61 GCATTGTACATAGGAAAATAGGAATATGAGACAGCACATTGT 108
 Db 340 GCATTGTACATAGGAAAATAGGAATATGAGACAGCACATTGT 387

RESULT 15

US-08-444-882-7

; Sequence 7, Application US/08444882

; Patent No. 5622705

; GENERAL INFORMATION:

; APPLICANT: Morrow, Casey D.

; TITLE OF INVENTION: ENCAPSULATED POLIOMYRUS NUCLEIC ACID AND METHODS OF MAKING AND

; TITLE OF INVENTION: USING SAME

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: LAHIVE & COCKFIELD

; STREET: 60 STATE STREET, SUITE 510

; CITY: BOSTON

; STATE: MASSACHUSETTS

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/444, 882

FILING DATE: 19-MAY-1995

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/087, 009

FILING DATE: 01-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Geary III, William C.

REGISTRATION NUMBER: 31,319

REFERENCE/DOCKET NUMBER: UAG-004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 1568 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 7..11565

US-08-444-882-7

Query Match 98.5%; Score 106.4; DB 1; Length 1568;

Best Local Similarity 99.1%; Pred. No. 5.1e-24;

Matches 107; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGTACAAGCCAAACATAACAGAAAAAGTATCCGATCCAGAGGACAGGGAGA 60
 Db 280 TGTACAAGCCAAACATAACAGAAAAAGTATCCGATCCAGAGGACAGGGAGA 339

QY 61 GCATTGTACATAGGAAAATAGGAATATGAGACAGCACATTGT 108
 Db 340 GCATTGTACATAGGAAAATAGGAATATGAGACAGCACATTGT 387

Result No.	Score	Query	Match	Length	DB ID	Description
1	129	100.0	2945	6	5462872-1	Patent No. 5462872
2	129	100.0	8932	3	US-09-124-900-1	Sequence 1, Appli
3	129	100.0	8933	3	US-08-463-210-A-3	Sequence 4, Appli
4	129	100.0	8933	3	US-09-620-958A-3	Sequence 3, Appli
5	129	100.0	8933	3	US-09-620-958A-4	Sequence 4, Appli
6	129	100.0	8933	3	US-09-620-958A-9	Sequence 9, Appli
7	129	100.0	8933	4	US-08-463-028-A-4	Sequence 4, Appli
8	127.4	98.8	1596	3	US-08-388-353-51	Sequence 651, Appli
9	127.4	98.8	1596	4	US-08-488-551B-651	Sequence 651, Appli
10	127.4	98.8	2696	4	US-09-325-131B-1	Sequence 1, Appli
11	127.4	98.8	2730	3	US-08-728-122-1	Sequence 1, Appli
12	127.4	98.8	2940	2	US-08-418-848A-3	Sequence 2, Appli
13	127.4	98.8	3426	2	US-08-418-848A-2	Sequence 2, Appli
14	127.4	98.8	3480	2	US-08-418-848A-4	Sequence 4, Appli
15	127.4	98.8	3721	2	US-08-418-848A-5	Sequence 6, Appli
16	127.4	98.8	3993	2	US-08-418-848A-6	Sequence 7, Appli
17	127.4	98.8	4059	2	US-08-418-848A-7	Sequence 8, Appli
18	127.4	98.8	4632	2	US-08-418-848A-8	Sequence 9, Appli
19	127.4	98.8	7399	2	US-08-418-848A-9	Sequence 5, Appli
20	127.4	98.8	9709	2	US-08-188-583-5	Sequence 1, Appli
21	127.4	98.8	9709	3	US-08-388-353-1	Sequence 1, Appli
22	127.4	98.8	9709	3	US-08-488-551B-1	Sequence 15, Appli
23	127.4	98.8	9709	4	US-09-309-572-15	Sequence 15, Appli
24	127.4	98.8	9709	4	US-09-718-096-15	Sequence 15, Appli
25	127.4	98.8	12479	4	US-09-318-138-13	Sequence 13, Appli
26	127.4	98.8	12494	3	US-08-935-312-13	Sequence 13, Appli
27	127.4	98.8	12494	3	US-08-848-760B-33	Sequence 33, Appli

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OM nucleic - nucleic search, using SW mode.

Run on: March 11, 2004, 20:30:23 ; Search time 65.0917 Seconds

1099.812 Million cell updates/sec

Title: US-10-003-035-75

Perfect score: 129

Sequence: 1 ttattccataatgtataggtagg.....acctccaaatcccgaaaa 129

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:
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3: /cn2_6_ptodata/2/ina/6A_COMB_seq:
4: /cn2_6_ptodata/2/ina/6B_COMB_seq:
5: /cn2_6_ptodata/2/ina/FACTUS_COMB_seq:
6: /cn2_6_ptodata/2/ina/backilesi_seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

%
RESULTS

RESULT 1
5462872-1

; Patent No. 5462872
; APPLICANT: Jonak, Zdenka L.; Debouchk, Christine; Clark, Robert
; TRULLI, Stephen
; TITLE OF INVENTION: HUMAN LYMPHOID CELLS EXPRESSING HUMAN
IMMUNODEFICIENCY VIRUS ENVELOPE PROTEIN GP160
; NUMBER OF SEQUENCES: 1
; CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,128
; FILING DATE: 08-OCT-1993
; PRIOR APPLICATION DATA:
APPLICATION NUMBER: 906,613
; FILING DATE: 30-JUN-1992
; APPLICATION NUMBER: 50,011
; FILING DATE: 24-SEP-1990
; SEQ ID NO:1:
5462872-1 LENGTH: 2945

ALIGMENTS

RESULT 2
US-09-124-900-1

; Sequence 1, Application US/09124900
; GENERAL INFORMATION:
; APPLICANT: KATINGER, Hermann
; BUCHACHER, Andrea
; APPLICANT: ERNST, Wolfgang
; APPLICANT: BALLAUN, Claudia
; APPLICANT: PERTSCHER, Martin
; APPLICANT: TRKOLA, Alexandra
; APPLICANT: FREDL, Renate
; APPLICANT: SCHMIDT, Christine

APPLICANT: KLIMA, Annelies
 APPLICANT: SPINDL, Franz
 APPLICANT: MUSTER, Thomas
 TITLE OF INVENTION: HIV-Vaccines
 FILE REFERENCE: 1939-112P
 CURRENT APPLICATION NUMBER: US/09/124,900
 CURRENT FILING DATE: 1998-07-30
 PRIOR APPLICATION NUMBER: PCT/EP95/01481
 PRIOR FILING DATE: 1995-04-19
 NUMBER OF SEQ ID NOS: 11
 SEQ ID NO: 1
 LENGTH: 8932
 TYPE: DNA
 ORGANISM: Human immunodeficiency virus type 1
 US-09-124-900-1

Query Match 100.0% Score 129; DB 3; Length 8932;
 Best Local Similarity 100.0%; Pred. No. 5.7e-33;
 Matches 129; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 TTATCATAATGATAGTAGGGCTGGTGTAAAGATAAGTTTGCTGTACTTCT 60
 Db 7629 TTATTCAATGATAGACTAGGGCTGGTGTAAAGATAAGTTTGCTGTACTTCT 7688

Qy 61 GTAGTGAAATASAGTTAGGCAAGGATATTACCAATTATCGTTCAAGCCACCTCCAACT 120
 Db 7689 GTAGTGAAATAGGTTAGGCAAGGATATTACCAATTATCGTTCAAGCCACCTCCAACT 7748

Qy 121 CCGAGGGGA 129
 Db 7749 CGAGGGGA 7757

RESULT 3
 US-08-463-210-4
 Sequence 4, Application US/08463210

GENERAL INFORMATION:
 APPLICANT: CHANG, Nancy T.
 APPLICANT: GALLI, Robert C.
 APPLICANT: WONG-STAL, Flossie
 TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Finneghan, L.L.P.
 STREET: 345 Park Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10154-0053

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy diskible
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: ParentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 416
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/693, 866
 FILING DATE: 23-JAN-1985
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/659, 339
 FILING DATE: 10-OCT-1984

ATTORNEY/AGENT INFORMATION:
 NAME: Serunian, Leslie A.
 REGISTRATION NUMBER: 35,353
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8933 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: HTLV-III
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1..8933
 OTHER INFORMATION: /standard name= "Clone BH10"
 OTHER INFORMATION: /not= "Corresponds to nucleotide positions 222 to 8933 in Figure 3 of EP 85307260"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 113..1648
 OTHER INFORMATION: /product= "gag"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 1408..4452
 OTHER INFORMATION: /product= "pol"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 4367..4975
 OTHER INFORMATION: /product= "sor"

FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 5560..8148
 OTHER INFORMATION: /product= "env"

US-08-463-210-4

Query Match 100.0% Score 129; DB 3; Length 8933;
 Best Local Similarity 100.0%; Pred. No. 5.7e-33;
 Matches 129; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 TTATCATAATGATAGTAGGGCTGGTGTAAAGATAAGTTTGCTGTACTTCT 60
 Db 7630 TTATTCATAATGATAGGGCTGGTGTAAAGATAAGTTTGCTGTACTTCT 7689

Qy 61 GTAGTGAAATAGGTTAGGCAAGGATATTACCAATTATCGTTCAAGCCACCTCCAACT 120
 Db 7690 GTAGTGAAATAGGTTAGGCAAGGATATTACCAATTATCGTTCAAGCCACCTCCAACT 7748

Qy 121 CCGAGGGGA 129
 Db 7750 CGAGGGGA 7758

RESULT 4
 US-09-620-958A-3
 Sequence 3, Application US/09620958A
 Patent No. 6294318

GENERAL INFORMATION:
 APPLICANT: Numonura, Kiyourada
 TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
 FILE REFERENCE: GP104-02.U7
 CURRENT APPLICATION NUMBER: US/09/620,958A
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 9
 SOFTWARE: FastSEQ For Windows Version 3.0
 SEQ ID NO: 3
 LENGTH: 8933
 TYPE: RNA
 ORGANISM: Human Immunodeficiency Virus
 FEATURE:
 NAME/KEY: source
 LOCATION: (1)...(8933)
 OTHER INFORMATION: Sequence of transcripts produced from the BH10
 Patent No. 6294318
 OTHER INFORMATION: plasmid.

US-09-620-958A-3

Query Match 100.0% Score 129; DB 3; Length 8933;
Best Local Similarity 67.4%; Pred. No. 5.7e-33;
Matches 87; Conservative 42; Mismatches 0; Indels 0; Gaps 0;

FEATURE:
ORGANISM: Artificial Sequence
OTHER INFORMATION: Sequence of the IAC-BsrC pseudo target
Patent No. 6294338

NAME/KEY: mutation
LOCATION: (4140)..(4159)
OTHER INFORMATION: Mutated positions: 4140-42, 4145-47, 4152,
OTHER INFORMATION: 4156-57, 4159

US-09-620-958A-9

Query Match 100.0% Score 129; DB 3; Length 8933;
Best Local Similarity 67.4%; Pred. No. 5.7e-33;
Matches 87; Conservative 42; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAATCATATGATAGTAGGGAGCTTGAAGATAAGTTTGCTGTACTTCT 60
Db 7630 UUAUCAUAGAUAGUAGUAGGAGCTGUAGGTUAGAAUAGCUNUUGCUACUUCU 7689

Qy 61 GTAGTGAATAGACTAGGGAGGATATTACCAATTATGTTCAAGCCACCTCCAAATC 120
Db 7690 GUASUGAAUAGAUAGGAGGAAUAUTACCACAUUAUCGGUTUAGACCCACCUCCAAUC 7749

Qy 121 CCGAGGGGA 129
Db 7750 CCGAGGGGA 7758

RESULT 5

US-09-620-958A-4

Sequence 4, Application US/09620958A
Patent No. 6294338

GENERAL INFORMATION:
APPLICANT: Numomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02-UT
CURRENT APPLICATION NUMBER: US/09/620-958A
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Fast-SEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 8933

TYPE: RNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence of the IAC-Asrc pseudo target
Patent No. 6294338

NAME/KEY: mutation
LOCATION: (4135)..(4155)
OTHER INFORMATION: Mutated positions: 4135, 4140-1, 4145, 4150,
OTHER INFORMATION: 4152-3, 4155

US-09-620-958A-4

Query Match 100.0% Score 129; DB 3; Length 8933;
Best Local Similarity 67.4%; Pred. No. 5.7e-33;
Matches 87; Conservative 42; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTAATCATATGATAGTAGGGAGGATATTACCAATTATGTTCAAGCCACCTCCAAATC 60
Db 7630 UUAUCAUAGAUAGUAGUAGGAGCTGUAGGTUAGAAUAGCUNUUGCUACUUCU 7689

Qy 61 GTAGTGAATAGACTAGGGAGGATATTACCAATTATGTTCAAGCCACCTCCAAATC 120
Db 7690 GUASUGAAUAGAUAGGAGGAAUAUTACCACAUUAUCGGUTUAGACCCACCUCCAAUC 7749

Qy 121 CCGAGGGGA 129
Db 7750 CCGAGGGGA 7758

RESULT 7

US-08-463-028-4

Sequence 4, Application US/08463028A
Patent No. 6610476

GENERAL INFORMATION:
APPLICANT: CHANG, Nancy T.
APPLICANT: GALLO, Robert C.
APPLICANT: WONG-STALL, Flossie
TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
STREET: 345 Park Avenue
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10154-0053

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,028
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/693,866
FILING DATE: 23-JAN-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/659,339

ATTORNEY/AGENT INFORMATION:
NAME: Serurian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4193US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-6400
TELEFAX: (212) 751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8933 base pairs
TYPE: nucleic acid

RESULT 6

US-09-620-958A-9

Sequence 9, Application US/09620958A
Patent No. 6294338

GENERAL INFORMATION:
APPLICANT: Numomura, Kiyotada
TITLE OF INVENTION: POLYNUCLEOTIDE AMPLIFICATION METHOD
FILE REFERENCE: GP104-02-UT
CURRENT APPLICATION NUMBER: US/09/620-958A
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Fast-SEQ for Windows Version 3.0

STRANDEDNESS: single
 TOPOLOGY: linear
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: HTLV-III
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..833
 OTHER INFORMATION: /standard_name="Clone BH10"
 /note= "Corresponds to nucleotide positions 222 to
 OTHER INFORMATION: 9154 in figure 3 of EP 85307260"
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 113..1648
 OTHER INFORMATION: /product= "gag"
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 1408..4452
 OTHER INFORMATION: /product= "pol"
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 4367..4975
 OTHER INFORMATION: /product= "sor"
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 5560..8148
 OTHER INFORMATION: /product= "env"
 US-08-463-028-4

Query Match 100..0%; Score 129; DB 4; Length 8933;
 Best Local Similarity 100..0%; Pred. No. 5..78..33;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTTTCAATAGTAACTGAGGTGGTAGGTAAAGATAAGTTGGTGTACTTT 60
 Db 7630 TTATCATAATGATGTTGAGGTGGTAGGTGGTAGGTAAAGATAAGTTGGTGTACTTT 7689
 Qy 61 GTAGTCATAATGAGTTGGCAGGGATTACCAATTGTTTCAAGACCCACCTCCAATC 120
 Db 7690 GTAGTCATAATGAGTTGGCAGGGATTACCAATTGTTTCAAGACCCACCTCCAATC 7749
 Qy 121 CCGAGGGAA 129
 Db 7750 CCGAGGGAA 7758

RESULT 8
 US-08-388-353-651
 / Sequence 651, Application US/08388353
 / Patent No. 6010895
 GENERAL INFORMATION:
 / APPLICANT: Descom, Nicholas J.
 / APPLICANT: Leamont, Jennifer C.
 / APPLICANT: McPhee, Dale A.
 / APPLICANT: Crowe, Suzanne
 / APPLICANT: Cooper, David
 / APPLICANT: Cooper, David
 TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 NUMBER OF SEQUENCES: 800
 CORRESPONDENCE ADDRESS:
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 ZIP: 11530
 COUNTRY: United States

RESULT 9
 US-08-468-551B-651
 / Sequence 651, Application US/08468551B
 / Patent No. 6015661
 GENERAL INFORMATION:
 / APPLICANT: Nicholas J. Deacon
 / APPLICANT: Dale A. McPhee
 / APPLICANT: David Cooper
 / TITLE OF INVENTION: NON-PATHOGENIC STRAINS OF HIV-1
 NUMBER OF SEQUENCES: 841
 CORRESPONDENCE ADDRESS:
 / ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 / STREET: 400 GARDEN CITY PLAZA
 / CITY: GARDEN CITY
 / STATE: NEW YORK
 / ZIP: 11530-0299
 / COUNTRY: U.S.A.
 COMPUTER READABLE FORM:
 / MEDIUM TYPE: FLOPPY disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/488,551B
 / FILING DATE: 14-FEB-1994
 / APPLICATION NUMBER: PM4002 (AU)
 / FILING DATE: 07-JUN-1995
 / APPLICATION NUMBER: PM3864 (AU)
 / FILING DATE: 14-FEB-1994
 / APPLICATION NUMBER: PN0284 (AU)
 / FILING DATE: 21-FEB-1994
 / APPLICATION NUMBER: PM3864 (AU)
 / FILING DATE: 14-FEB-1995
 / APPLICATION NUMBER: PN3021/95
 / FILING DATE: 17-MAY-1995
 / ATTORNEY/AGENT INFORMATION:

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/388,353

NAME: FRANK S. DIGILIO
 REFERENCE/DOCKET NUMBER: 9606Z
 TELEPHONE: (516) 742-4343
 TELEX/FAX: (516) 742-4366
 INFORMATION FOR SEQ ID NO: 651:
 SEQUENCE CHARACTERISTICS:
 TYPE: 1596 base pairs
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-08-488-551B-651

Query Match 98.8%; Score 127.4; DB 3; Length 1596;
 Best Local Similarity 99.2%; Pred. No. 1.1e-32;
 Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTATTATAATGATAGTAGGAGGGCTTAAAGATAAGTTTGCTGTACTTCT 60
 Db 193 TTATTATAATGATAGTAGGAGGGCTTAAAGATAAGTTTGCTGTACTTCT 252

Qy 61 GTAGTGAATAGTAGTTAGGCAGGGATATTACCAATTATGGTTTCAGACCCACCTCCAAATC 120
 Db 253 ATAGTGAATAGTAGTTAGGCAGGGATATTACCAATTATGGTTTCAGACCCACCTCCAAATC 312

Qy 121 CCGAGGGGA 129
 Db 313 CCGAGGGGA 321

RESULT 10
 US-09-325-131B-1

Sequence 1, Application US/09325131B
 Patent No. 6592104
 GENERAL INFORMATION:
 APPLICANT: CLOUD, MILES W.
 ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION: DETECTION OF HIV INFECTION
 FILE REFERENCE: UMSG:234
 CURRENT APPLICATION NUMBER: US/09/325,131B
 PRIORITY FILING DATE: 1999-06-08
 PRIOR APPLICATION NUMBER: 08/143,168
 PRIORITY FILING DATE: 1996-10-09
 PRIORITY FILING DATE: 1993-10-26
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 1
 LENGTH: 2696
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-325-131B-1

Query Match 98.8%; Score 127.4; DB 4; Length 2696;
 Best Local Similarity 99.2%; Pred. No. 1.3e-32; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TTATTATAATGATAGTAGGAGGGCTTAAAGATAAGTTTGCTGTACTTCT 60
 Db 2489 TTATTATAATGATAGTAGGAGGGCTTAAAGATAAGTTTGCTGTACTTCT 2548

Qy 61 GTAGTGAATAGTAGTTAGGCAGGGATATTACCAATTATGGTTTCAGACCCACCTCCAAATC 120
 Db 2549 GTAGTGAATAGTAGTTAGGCAGGGATATTACCAATTATGGTTTCAGACCCACCTCCAAAC 2608

Qy 121 CCGAGGGGA 129
 Db 2609 CCGAGGGGA 2617

RESULT 12
 US-08-418-848A-3

Sequence 3, Application US/08418848A
 Patent No. 5847056
 GENERAL INFORMATION:
 APPLICANT: SCHUBERT, MANFRED, HARMISON II, CHEN, BANJERJEA, AKHIL
 ATTORNEY/AGENT INFORMATION:
 TITLE OF INVENTION: DEFECTIVE, INTERFERING HIV PARTICLES
 NUMBER OF SEQUENCES: 77
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNegan, L.L.P.
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 COUNTRY: U.S.A.

RESULT 11

ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/418,848A
 FILING DATE: 07-APR-1995
 CLASSIFICATION: 526
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/936,849
 FILING DATE: 28-AUG-1992
 CLASSIFICATION: 526
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4091US2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-4800
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2940 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 US-08-418-848A-3

Query Match 98.8%; Score 127.4; DB 2; Length 2940;
 Best Local Similarity 99.2%; Pred. No. 1.4e-32;
 Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Db 1552 1 TTATTCAATGATGAGTACTAGGGCTGGTAGGTAAAGATAAGTTGGTGTACTTCT 60

Qy 61 GTAGTGAATAGAGTACTAGGGCATTACCAATTGTTCAAGCCACCTCCAATC 1671
 Db 1612 ATAGTGAATAGAGTACTAGGGCATTACCAATTGTTCAAGCCACCTCCAATC 1671

Qy 121 CCGAGGGAA 129
 Db 1672 CCGAGGGAA 1680

RESULT 13
 US-08-418-848A-2
 / Sequence 2, Application US/08418848A
 / Patent No. 5847096
 GENERAL INFORMATION:
 APPLICANT: SCHUBERT, MANFRED, HARMISON II,
 ADDRESS: MORGAN & FINNEGAN, L.L.P.
 CITY: NEW YORK
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/418,848A
 FILING DATE: 07-APR-1995
 CLASSIFICATION: 526
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4091US2
 TELEPHONE: 212-758-4800
 TELEX: 421792

Query Match 98.8%; Score 127.4; DB 2; Length 3426;
 Best Local Similarity 99.2%; Pred. No. 1.4e-32;
 Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TTATTCAATGATGAGTACTAGGGCTGGTAGGTAAAGATAAGTTGGTGTACTTCT 60
 Db 1981 TTATTCAATGATGAGTACTAGGGCTGGTAGGTAAAGATAAGTTGGTGTACTTCT 2040

Qy 61 GTAGTGAATAGAGTACTAGGGCATTACCAATTGTTCAAGCCACCTCCAATC 120
 Db 2041 ATAGTGAATAGAGTACTAGGGCATTACCAATTGTTCAAGCCACCTCCAATC 2109

RESULT 14
 US-08-418-848A-4
 / Sequence 4, Application US/08418848A
 / Patent No. 5847096
 GENERAL INFORMATION:
 APPLICANT: SCHUBERT, MANFRED, HARMISON II,
 ADDRESS: MORGAN & FINNEGAN, L.L.P.
 CITY: NEW YORK
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 07/936,849
 FILING DATE: 28-AUG-1992
 CLASSIFICATION: 526
 ATTORNEY/AGENT INFORMATION:
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4091US2
 TELEPHONE: 212-758-4800
 TELEX: 421792

Query Match 98.8%; Score 127.4; DB 2; Length 3426;
 Best Local Similarity 99.2%; Pred. No. 1.4e-32;
 Matches 128; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 121 CCGAGGGAA 129
 Db 2101 CCGAGGGAA 2109

RESULT 15
 US-08-418-848A-5
 / Sequence 5, Application US/08418848A
 / Patent No. 5847096
 GENERAL INFORMATION:
 APPLICANT: SCHUBERT, MANFRED, HARMISON II,
 ADDRESS: MORGAN & FINNEGAN, L.L.P.
 CITY: NEW YORK
 ZIP: 10154
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 07/936,849
 FILING DATE: 28-AUG-1992
 CLASSIFICATION: 526
 ATTORNEY/AGENT INFORMATION:
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4091US2
 TELEPHONE: 212-758-4800
 TELEX: 421792

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 3190 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-418-848A-4

Query Match 98.8%; Score 127.4; DB 2; Length 3480;
 Best Local Similarity 99.2%; Pred. No 1.4e-32; Indels 0; Gaps 0;
 Matches 128; Conservative 0; Mismatches 1;

Db 1981 TTATTCAATGATACTGGAGGCTGGTAGGTAAAGAATAGTTTGGCTGTACTTCT 60
 Qy 61 GTAGTGAATAGACTTACCGGATATCACCATTATGGTTTCAAGACCCACCTCCCAATC 120
 Db 2041 ATAGTGAATAGACTTACCGGATATCACCATTATGGTTTCAAGACCCACCTCCCAATC 2100

Query Match 98.8%; Score 127.4; DB 2; Length 3480;
 Best Local Similarity 99.2%; Pred. No 1.4e-32; Indels 0; Gaps 0;
 Matches 128; Conservative 0; Mismatches 1;

Db 1991 TTATTCAATGATACTGGAGGCTGGTAGGTAAAGAATAGTTTGGCTGTACTTCT 60
 Qy 61 GTAGTGAATAGACTTACCGGATATCACCATTATGGTTTCAAGACCCACCTCCCAATC 120
 Db 2041 ATAGTGAATAGACTTACCGGATATCACCATTATGGTTTCAAGACCCACCTCCCAATC 2100

Search completed. March 11, 2004, 23:12:15
 Job time : 65.0917 secs

RESULT 15
 US-08-418-848A-5

Sequence 5, Application US/08418848A
 Patent No. 5847036

GENERAL INFORMATION:
 APPLICANT: SCHUBERT, MANFRED, HARMISON II,
 APPLICANT: GEORGE G., CHANG-JIE, CHEN, BANGERJEEA, AKHIL
 TITLE OF INVENTION: DEFECTIVE, INTERFERING
 NUMBER OF SEQUENCES: HIV PARTICLES
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
 STREET: 345 PARK AVENUE
 CITY: NEW YORK
 COUNTRY: U.S.A.
 ZIP: 10154

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM PC COMPATIBLE
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/418,848A
 FILING DATE: 07-APR-1995
 CLASSIFICATION: 526
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/936,849
 FILING DATE: 28-AUG-1992
 CLASSIFICATION: 526
 ATTORNEY/AGENT INFORMATION:
 NAME: RICHARD W. BORK
 REGISTRATION NUMBER: 36,459
 REFERENCE/DOCKET NUMBER: 2026-4091US2

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-758-4800
 TELEX: 421792
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3721 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-418-848A-5

Query Match 98.8%; Score 127.4; DB 2; Length 3721;
 Best Local Similarity 99.2%; Pred. No 1.5e-32;
 Matches 128; Conservative 0; Mismatches 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:52:43 ; Search time 806.349 Seconds
(without alignments)
6934.037 Million cell updates/sec

Title: US-10-003-035-75

Perfect score: 129
Sequence: 1 ttattccatgtatgtatgg.....accccaatcccgaggaa 129

Scoring table: IDENTITY_NUC
Gapext 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters:

6940544

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	129	100.0	861	6 I02160	I02160 Sequence 1
2	129	100.0	1026	6 I02162	I02162 Sequence 3
3	129	100.0	2237	6 I02028	DNA sequence
4	129	100.0	2552	6 I05789	Sequence 8
5	129	100.0	2945	6 AR365081	Sequence
6	129	100.0	3156	6 E01088	Nucleic acid
7	129	100.0	3156	14 HIVHXB3	M14100 Human immunodeficiency virus
8	129	100.0	8932	14 HIVBH102	M15654 Human immunodeficiency virus
9	129	100.0	8933	6 AR094659	Sequence
10	129	100.0	8933	6 AR382018	Sequence
11	129	100.0	8933	6 AX078307	Sequence
12	129	100.0	8933	6 AX078308	Sequence
13	129	100.0	8933	6 AX078313	Sequence
14	129	100.0	9748	6 E01099	E01099 DNA sequence
15	129	100.0	9748	14 REHTLV3	X01762 Human T-cell lymphotropic virus
16	129	100.0	9749	6 I07983	I07983 Sequence 1
17	129	100.0	9781	14 HIVEL2CG	Z11530 Human Immunodeficiency virus
18	129	100.0	9918	12 AF43044	Synthetic sequence
19	128	99.2	9795	14 HIVTH75A	L31963 Human immunodeficiency virus
20	127.4	98.8	2148	6 BD238379	BD238379 Virus vac
21	127.4	98.8	2148	6 AX032757	AX032757 Sequence
22	127.4	98.8	2264	6 I06771	I06771 Sequence 8
23	127.4	98.8	2559	14 AY426102	AY426102 HIV-1 isoform
24	127.4	98.8	2559	14 AY426103	AY426103 HIV-1 isoform
25	127.4	98.8	2559	14 AY426104	AY426104 HIV-1 isoform
26	127.4	98.8	2559	14 AY426105	AY426105 HIV-1 isoform
27	127.4	98.8	2559	14 AY426106	AY426106 HIV-1 isoform
28	127.4	98.8	2559	14 AY426107	AY426107 HIV-1 isoform
29	127.4	98.8	2559	14 AY426108	AY426108 HIV-1 isoform
30	127.4	98.8	2559	14 AY426109	AY426109 HIV-1 isoform
31	127.4	98.8	2562	6 AX166280	AX166280 Sequence
32	127.4	98.8	2565	6 BD000747	BD000747 Recombinant
33	127.4	98.8	2696	6 AR264703	AR264703 Sequence
34	127.4	98.8	2730	6 AR097865	Sequence
35	127.4	98.8	2940	6 AR064430	Sequence
36	127.4	98.8	3426	6 AR064429	Sequence
37	127.4	98.8	3480	6 AR064431	Sequence
38	127.4	98.8	3721	6 AR064432	Sequence
39	127.4	98.8	3993	6 AR064433	Sequence
40	127.4	98.8	4059	6 AR064434	Sequence
41	127.4	98.8	4632	6 AR064435	Sequence
42	127.4	98.8	6229	6 BD238380	Virus vac
43	127.4	98.8	6229	6 AX032758	AX032758 Sequence
44	127.4	98.8	7399	6 AR064436	AR064436 Sequence
45	127.4	98.8	9000	14 HIVU26942	U26942 Human immunodeficiency virus

ALIGNMENTS

RESULT	1	10160	LOCUS	Sequence 1 from Patent US 4861707.	linear	PAT	21-MAY-1993
DEFINITION							
ACCESSION							
VERSION							
KEYWORDS							
SOURCE							
ORGANISM							
Unclassified							
Unclassified	1 (bases 1 to 861)						
REFERENCE	Ivanoff, L.A. and Pettaway, S.R.						
AUTHORS							
TITLE	Human immunodeficiency virus antigen						
JOURNAL	Patent: US 4861707-A 1 29-Aug-1989; E. I. Du Pont de Nemours and Company; Wilmington, DE						

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

FEATURES	Location/Qualifiers	AUTHORS	Nozaki, C., Matsushita, S., Hattori, T. and Takatsuki, K.
source	1 .861 /mol_type="unassigned DNA"	TITLE	HIV FUSED PROTEIN
		JOURNAL	CHENO SERO THERAPEUT RES INST
ORIGIN		COMMENT	JP 1989179687-A 1 17-JUL-1989;
		PN	JP 1989179687-A/1
Query Match	Score 129; DB 6; Length 861;	PD	PD 17-JUL-1989
Best Local Similarity 100.0%	Pred. No. 4.2e-28;	PP	PP 30-DEC-1987 JP 19897336292
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		PI	PI NOZAKI CHIKAHIDE, MATSUISHITA SHUZO, HATTORI TOSHIRO, PI
Qy	1 TTATTCATAATGATAGTAGGTAGGGCTTGGTAGGTTAAGATAAGTGTACTTCT 60	PC	TAKATSUKI KIYOSHI
Db	655 TTATTCATAATGATAGTAGTAGGGCTTGGTAGGTTAAGATAAGTGTACTTCT 714	PC	C12N7/04, C07K13/00, C12P21/02//A61K39/21, C12N15/00, (C12P21/02,
Qy	61 GTAGTGAAATAGAGTTAGCCAGGGATAATTACCAATTATCGTTTCAGACCCACCTCCAAATC 120	PC	(C12R1/91;
Db	715 GTAGTGAAATAGAGTTAGCCAGGGATAATTACCAATTATCGTTTCAGACCCACCTCCAAATC 774	CC	(C12N15/00, C12R1/91);
Qy	121 CGGAGGGAA 129	CC	strandedness: Double;
Db	775 CGGAGGGAA 783	topology: Linear;	
		CC	hypothetical: No;
		CC	anti-sense: No;
		CC	*source: clone=Plasmid lambdaBH10;
		FH	Key
		FH	Location/Qualifiers
		FT	1 .2130
		FT	/product='gag-env hybrid protein' FT 3 'UTR
		2131 .2237	
		Location/Qualifiers	
		1 .2237	
		/organism="Homo sapiens"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:9606"	
FEATURES	Source	ORIGIN	
RESULT 2		Query Match	100.0%; Score 129; DB 6; Length 2237;
LOCUS	I02162 1026 bp ss-DNA	Best Local Similarity	100.0%; Pred. No. 4e-28;
DEFINITION	Sequence 3 from Patent US 4861707.	Matches	129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	I02162	ORIGIN	
VERSION	102162.1 GI:270318	Qy	1 TTATTCATAATGATAGTAGGGCTTGGTAGGTTAAGATAAGTGTACTTCT 60
KEYWORDS	Unknown.	Db	1609 TTATTCATAATGATAGTAGGGCTTGGTAGGTTAAGATAAGTGTACTTCT 1668
SOURCE	Unclassified.	Qy	61 GTAGTGAAATAGAGTTAGCCAGGGATAATTACCAATTATCGTTTCAGACCCACCTCCAAATC 120
ORGANISM		Db	1669 GTAGTGAAATAGAGTTAGCCAGGGATAATTACCAATTATCGTTTCAGACCCACCTCCAAATC 1728
REFERENCE	1 (bases 1 to 1026)	Qy	121 CGGAGGGAA 129
AUTHORS	Ivanoff, J.L.A. and Peteway, S.R.	Db	1729 CGGAGGGAA 1737
TITLE	Human immunodeficiency virus antigen	RESULT 4	
JOURNAL	Patent: US 4861707-A 3 29-AUG-1989;	LOCUS	I05789
	E. I. Du Pont de Nemours and Company; Wilmington, DE	DEFINITION	Sequence 8 from Patent EP 0272858.
FEATURES	Location/Qualifiers	ACCESSION	I05789
source	1 .1026	VERSION	I05789 1 GI:590911
	/organism="unassigned DNA"	KEYWORDS	
	/mol_type="unassigned DNA"	SOURCE	Unknown.
ORIGIN		ORGANISM	Unclassified.
Query Match	Score 129; DB 6; Length 1026;	REFERENCE	1 (bases 1 to 2552)
Best Local Similarity 100.0%	Pred. No. 4.1e-28;	AUTHORS	Rusche, J.J., Carson, H., Putney, S. and Jellis, C.L.
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		TITLE	Recombinant HIV envelope proteins produced in insect cells
Qy	1 TTATTCATAATGATAGTAGGGCTTGGTAGGTTAAGATAAGTGTACTTCT 60	JOURNAL	Patent: EP 0272858-A2 8 29-JUN-1988;
Db	820 TTATTCATAATGATAGTAGGGCTTGGTAGGTTAAGATAAGTGTACTTCT 879	FEATURES	Location/Qualifiers
Qy	61 GTAGTGAAATAGAGTTAGCCAGGGATAATTACCAATTATCGTTTCAGACCCACCTCCAAATC 120	source	1 .2552
Db	880 GTAGTGAAATAGAGTTAGCCAGGGATAATTACCAATTATCGTTTCAGACCCACCTCCAAATC 939		/organism="unassigned DNA"
Qy	121 CGGAGGGAA 129		
Db	940 CGGAGGGAA 948	ORIGIN	
RESULT 3		Query Match	100.0%; Score 129; DB 6; Length 2552;
LOCUS	E02028 2237 bp DNA linear	Best Local Similarity	100.0%; Pred. No. 4e-28;
DEFINITION	DNA sequence coding for gag-env hybrid protein.	Matches	129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	E02028	ORIGIN	
VERSION	GI:2170276	Qy	1 TTATTCATAATGATAGTAGGGCTTGGTAGGTTAAGATAAGTGTACTTCT 60
KEYWORDS	JP 1989179687-A/1.	Db	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
SOURCE	Homo sapiens (human)	ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ORGANISM		REFERENCE	1 (bases 1 to 2237)

Qy 61 GTAGTGAATAGAGTTAGCCAGGGATATTACCAATTATCGTTTCAGACCCACTCCCAATC 120
 Db 2095 GTAGTGAATAGACTTAGCCAGGGATATTACCAATTATCGTTTCAGACCCACTCCCAATC 2154
 Qy 121 CGAGGGAA 129
 Db 2155 CGAGGGAA 2163

RESULT 5
 AR365081 AR365081 2945 bp DNA linear PAT 03-SEP-2003
 DEFINITION Sequence 1 from patent US 5462872.
 VERSION AR365081.1 GI:34428384
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.

REFERENCE 1. /bases 1 to 2945)
 AUTHORS Jonak, Z.L., Dabouck, C., Clark, R. and Trulli, S.
 TITLE Human lymphoid cells expressing human immunodeficiency virus
 envelope protein GPI60
 JOURNAL Patent: US 5462872-A 1 31-OCT-1995;
 FEATURES Location/Qualifiers 1..2945
 source /organism="Unknown"
 /mol_type="genomic DNA"

ORIGIN Query Match Score 129; DB 6; Length 3156;
 Best Local Similarity 100.0%; Pred. No. 3..9e-28;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TTAATTCAATGATAGAGGGATTTAGGTAGTTAAGATAGTTGACTTCT 60
 Db 2327 TTAATTCAATGATAGAGGGATTTAGGTAGTTAAGATAGTTGACTTCT 60

RESULT 6
 HIVHXB3 HIVHXB3 3156 bp ss-RNA linear VRL 02-AUG-1993
 LOCUS Human immunodeficiency virus type 1, isolate HXB3, env region.
 DEFINITION Human immunodeficiency virus type 1, isolate HXB3, env region.
 ACCESSION M14100
 VERSION M14100..1 GI:327751
 KEYWORDS Human immunodeficiency virus 1 (HIV-1)
 SOURCE Lentivirus group.
 ORGANISM Human immunodeficiency viruses; Retroviridae; Lentiviruses; Primate
 Viruses; Retrovirus; Retroviridae

REFERENCE 1. (bases 1 to 3156)
 AUTHORS Crowl, R., Ganguly, K., Gordon, M., Conroy, R., Schaber, M., Kramer, R.,
 Shaw, G., Wong-Staal, F. and Reddy, B.P.
 TITLE HTLV-III env gene products synthesized in E. coli are recognized by
 antibodies present in the sera of AIDS patients
 JOURNAL Cell 41 (3), 979-986 (1985)
 MEDLINE 85228248
 PUBMED 2988795
 COMMENT Original source text: Human immunodeficiency virus type 1 (HIV-1),
 isolate HXB3, proviral DNA.
 FEATURES Location/Qualifiers 1..3156
 source /organism="Human immunodeficiency virus 1"
 /mol_type="Genomic RNA"
 /db_xref="Taxon:11676"
 prim_transcript <1..>3156
 prim_transcript <1..>3156
 CDS /note="partial"
 /note="tat, rev, nef subgenomic mRNA"
 <1..51

REFERENCE 1. (bases 1 to 3156)
 AUTHORS Robaato, M.K., Robaato, C.G., Eragamu, P.R., Jiyooji, M.S. and
 Eurotashii, I.U.
 DEFINITION Nucleic acid sequence coding for HTLV envelop protein.
 ACCESSION E01088
 VERSION E01088..1 GI:2169347
 SOURCE Patent: JP 1987012799-A/1.
 ORGANISM unidentified
 unidentified unidentified
 unidentified unidentified
 unidentified unidentified
 unidentified unidentified
 unidentified unidentified

RESULT 6
 E01088 E01088 3156 bp DNA linear PAT 29-SEP-1997
 DEFINITION Envelope protein of virus of acquired immunodeficiency syndrome
 ENVIRONMENT
 ACCESSION E01088..1 GI:2169347
 VERSION JP 1987012799-A/1.
 SOURCE Patent: JP 1987012799-A/1.
 ORGANISM OS Human (Homo sapiens)
 PN JP 1987012799-A/1
 PD 21-JAN-1987
 PF 18-APR-1986 JP 1986089830
 PR 19-APR-1985 US 85 725021
 PI ROBAATO MITSUCHI KUROURU, ROBAATO CHIYAARUU GARO, PI FUOTSUSHII
 ERAGAMU PUREMKUMA REDEI, JIYOOJI METSUDO SHIYOU, PI FUOTSUSHII
 IICHINGU UNGUOSUTAARU
 PC C07K13/00, A61K39/21, C07H21/04, C12N15/00, C12P21/00, PC

/translation="ILQQLLFFHFQNWNST"
<1..33
/note="tat, rev, nef subgenomic mRNA intron 1"
34..301
/note="tat protein, (first expressed exon)"
/number=2
join(87..301,2632..2677)
/note="tat protein"
/codon_start=1
/protein_id="AAA44676.1"
/db_xref="GI:322753"
/translation="MPEPVDPLPEPKWPKPSQPKTACTCNCKKKCFCPHQCVCFTKALG
ISYGRKGERQRREPPQGQTHQYVSLSKOPTSRSRQDPTGPKE"
join(226..301,2632..2906)
/note="rev protein"
/codon_start=1
/protein_id="AAA44677.1"
/db_xref="GI:322754"
/translation="MAGRSQDSDEDLKAVRIJKFLYQSNNPPNPESTRQARNRRRR
WRQRORHSSRILSTYLGRSAEPVPLQQLPPLERLTLDNCNEDCGTSGTQGVGSQI
LVSPTLIESGATE"
302..261
/note="tat cds intron 2"
318..563
/note="rpu protein"
/codon_start=1
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/db_xref="GI:322755"
/translation="MQPIQIAITVALVVAIIIAIVVVWSIVITIBYRKILQRKIDRLLDR
LIPIRAEDSGNESEGEISALVEMGVGMGHAPDVDDI"
478..3048
/note="envelope polyprotein"
/codon_start=1
/protein_id="AAA44679.1"
/db_xref="GI:322756"
/translation="MRYVEKYKQHLMRWRNGRMGTMMLGMLMICSATERKLWVTTYYGVPV
WKEATTTFCASDAKAYDTEEVNWNTAAGVPPDPDNEQUNLVNTENEMMKNDMVE
OMBEDIISWMDQSIKPCVYLTPUCVLKCTDLDKNDTNTSSGRMMEKGIEKNCSEN
TSPSIRGKVKQKEYAFFYKCLIDTIDNDTSTSUTSCNTSVTOACPVSFETIPYC
APAGRAALKCNNTDENGPGCPNTSYVOTCHERPVYSTOOLLNSLAEEFVYRSON
PTDNAKTLIVQLQNLTSVEINCPTNNTKKRQGPERAFVTTGKGNMRQAHCNLIS
RAKMNNTKQIASKNLREQFNNTKTIIFQSSGSDPELYTHSNPGFFYCNSTQLFN
STWNNTSTSTEGNNNTTESSDTTLPCKIKOFNMWQEVGKANYAPPISOQTCSSNT
GLLITRDGGANNNNGSEIIPRGGGMDRNWLSYKIVKVKBGPVTAKGRRVQQR
EKEAVGIGALFLGLGAAGSTMGAASTMLTVQAROLUSGIVQOONNLRAIAQQHLL
QLTWGIQQLQARILAVERYLKLQOQLLGIWGCGKLICCTATAEWNAIWSNKSLQEWLN
KLTWMEWDDEINNTSLIHSLSQNOQNLLELDLWLNINWLWLT
DREDSIRLYNGSLALIIDLRLSCLFSTYRVRQYSPSFQTHLPPIRGDPDEBGEIGER
exon
2632..>2906
/note="rev protein"
2632..>2777
/note="tat protein"
/codon_start=1
/protein_id="AAA44680.1"
/db_xref="GI:554954"
/translation="IMGGRKISKSSVVGPAVRMRRAFPAAQDGVGAASR"
CDS
3050..>3156
/note="nef protein, partial"
/codon_start=1
/protein_id="AAA44680.1"
/db_xref="GI:554954"
/translation="TTATTCAATGATAGTAGAGGGCTTGAGTAGTTTAAAGATAAGTTTGCCTGACTTTCT
1 TTATTCAATGATAGTAGAGGGCTTGAGTAGTTTAAAGATAAGTTTGCCTGACTTTCT
Db
2527
Qy
1 GTAGTGAATGAGTTAGCCGGGATATTACCAATTGTTCAAGCTTCAAGCCACCTCCCCAACTC
2586
2655
2677
8
HIVBH102
LOCUS
DEFINITION Human immunodeficiency virus type 1, isolate BH10, genome.
ACCESSION M15654
VERSION M15654.1
KEYWORDS TAR region; acquired immune deficiency syndrome; env protein; gag protein; long terminal repeat (LTR); pol protein; polyprotein; proviral gene; reverse transcriptase; transactivator.
SEGMENT 2 of 2
SOURCE Human immunodeficiency virus 1 (HIV-1)
ORGANISM Human immunodeficiency virus 1
Viruses: Retroviridae; Lentiviridae; Primate lentivirus group.
REFERENCE (bases 1 to 8932)
AUTHORS Wong-Staal,F., Gallo,R.C., Chang,N.T., Ghayeb,J.J., Papas,T.S., Lautenberger,J.A., Pearson,M.L., Petteway,S.R.Jr., Ivanoff,F.L., Baumeister,K., Whitehorn,B.A., Rafalski,J.A., Doran,E.R., Joseph,S.J., Starcich,B., Liwak,K.J., Patarcic,R., Haseltine,W.A., and Ratner,L.
TITLE Complete nucleotide sequence of the AIDS virus, HTLV-III
JOURNAL Nature 313 (6000), 277-284 (1985)
MEDLINE 85111123
PUBMED 2578615
REFERENCE 2 (bases 1 to 8932)
AUTHORS van Beveren,C.P., Coffin,J. and Hughes,S.
TITLE Appendix B: HIV-3 genome
JOURNAL (Eds.); RNA TUMOR VIRUSES, MOLECULAR BIOLOGY OF TUMOR VIRUSES, SECOND EDITION, 2,
Cold Spring Harbor Laboratory, CSH, NY (1985)
REFERENCE 3 (sites)
AUTHORS Hostomtska,Z., Hudson,G.O., Moonaw,E.W. and Nodes,B.R.
TITLE Reconstitution in vitro of RNase H activity by using purified N-terminal and C-terminal domains of human immunodeficiency virus type 1 reverse transcriptase
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 88 (4), 1148-1152 (1991)
MEDLINE 9114229
PUBMED 1705027
COMMENT Original source text: Human immunodeficiency virus type 1 (HIV-1) proviral DNA clone BH10.
(in) Weiss,R., Teich,N., Varmus,H. and Coffin,J. (Eds.); RNA Tumor Virus, Molecule; review; bases 1 to 8932.
The BH10 sequence differs from BH8 and BH5 by 0.9% in the coding regions and 1.8% in the noncoding regions, and the authors of [1] believe that these are stable variants.
The HTLV-III genome encodes at least seven proteins: gag, pol, env, tat, trs, 27K antigen and the sox 23K product. The 3' ORF (positions 8153-873) is truncated in BH10 (stop codon at positions 8522-8524), but reads through in BH8 and other sequences to yield what is now called the 27K antigen.
The mechanism for pol gene translation has not been elucidated: a gag-pol fusion protein is possible; splicing or frameshift have not been ruled out. The viral protease would be determined by the region in question.
The Tat protein (trans-activator protein, approximately 14 kb) is an effector of an autostimulatory pathway through interaction with a positive control element, the trans-activating responsive sequence, TAR. Tat seems to be a transcriptional control molecule in HTLV-1, but is both that and a post-transcriptional regulatory molecule in HTLV-III. Deletion mutants in the tat gene are incapable of prolific replication and exhibit no cytopathic effects in T4+ cell lines.
In addition to the
9.4 kb genomic mRNA, subgenomic mRNAs of 7.4, 5.5, 5.0, 4.3, 2.0

QY 61 GTACTGAATAGAGTGTAGGAGGGATTACCAATTATCGTTTCAAGACCACCTCCAACTC 120
 Db 7689 GTACTGAATAGAGTGTAGGAGGGATTACCAATTATCGTTTCAAGACCACCTCCAACTC 7749

QY 121 CCGAGGGAA 129
 Db 7749 CCGAGGGAA 7757

RESULT 9
 AR094659 AR094659 8933 bp DNA linear PAT 08-SEP-2000
 LOCUS DEFINITION Sequence 4 from patent US 6001977.
 ACCESSION AR094659
 VERSION AR094659.1 GI:10021783
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 8933)
 AUTHORS Chang,N.T., Gallo,R.C. and Wong-Staal,F.
 TITLE Cloning and expression of HTLV-III DNA
 JOURNAL Patent: US 6001977-A 4 14-DEC-1999;
 FEATURES Location/Qualifiers 1_ 8933
 /mol type="unassigned DNA"
 source /mol type="unassigned DNA"
 ORIGIN Query Match 100.0%; Score 129; DB 6; Length 8933;
 Best Local Similarity 100.0%; Pred. No. 3.7e-28;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTCAATGATGATGAGTGTAGGGTAAAGATAAGTGTGTGACTTCT 60
 Db 7630 TTATTCAATGATGATGAGTGTAGGGTAAAGATAAGTGTGTGACTTCT 7689
 QY 61 GTACTGAATAGAGTGTAGGAGGGATTACCAATTATCGTTTCAAGACCACCTCCAACTC 120
 Db 7690 GTACTGAATAGAGTGTAGGAGGGATTACCAATTATCGTTTCAAGACCACCTCCAACTC 7749
 Qy 121 CCGAGGGAA 129
 Db 7750 CCGAGGGAA 7758

RESULT 10
 AR382018 AR382018 8933 bp DNA linear PAT 18-DEC-2003
 LOCUS DEFINITION Sequence 4 from patent US 6610476.
 ACCESSION AR382018
 VERSION AR382018.1 GI:40090419
 KEYWORDS Unknown.
 SOURCE Unclassified.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 8933)
 AUTHORS Chang,N.T., Gallo,R.C. and Wong-Staal,F.
 TITLE Detection of HIV-1 DNA
 JOURNAL Patent: US 6610476-A 4 26-AUG-2003;
 FEATURES Location/Qualifiers 1_ 8933
 /organism="unknown"
 source /mol type="genomic DNA"
 ORIGIN Query Match 100.0%; Score 129; DB 6; Length 8933;
 Best Local Similarity 100.0%; Pred. No. 3.7e-28;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTCAATGATGATGAGTGTAGGGTAAAGATAAGTGTGTGACTTCT 60
 Db 7630 TTATTCAATGATGATGAGTGTAGGGTAAAGATAAGTGTGTGACTTCT 7689

RESULT 11
 AX078307 AX078307 8933 bp RNA linear PAT 22-FEB-2001
 LOCUS DEFINITION Sequence 3 from Patent WO0107661.
 ACCESSION AX078307
 VERSION AX078307.1 GI:13157998
 KEYWORDS SOURCE Human immunodeficiency virus
 ORGANISM Human immunodeficiency virus
 Viruses; Retro viruses; Lentiviridae; Lentivirus; Primate
 lentivirus group.
 REFERENCE 1
 AUTHORS Nunomura,K.
 TITLE Polynucleotide amplification method
 JOURNAL Patent: WO 0107661-A 3 01-FEB-2001;
 Gen-Probe Incorporated (US)
 FEATURES Location/Qualifiers 1_ .8933
 /organism="Human immunodeficiency virus"
 /mol type="unassigned RNA"
 /db xref="taxon:12721"
 /note="Sequence of transcripts produced from the BH10
 plasmid."
 ORIGIN Query Match 100.0%; Score 129; DB 6; Length 8933;
 Best Local Similarity 100.0%; Pred. No. 3.7e-28;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTCAATGATGATGAGTGTAGGGTAAAGATAAGTGTGTGACTTCT 60
 Db 7630 TTATTCAATGATGATGAGTGTAGGGTAAAGATAAGTGTGTGACTTCT 7689
 QY 61 GTACTGAATAGAGTGTAGGAGGGATTACCAATTATCGTTTCAAGACCACCTCCAACTC 120
 Db 7690 GTACTGAATAGAGTGTAGGAGGGATTACCAATTATCGTTTCAAGACCACCTCCAACTC 7749

RESULT 12
 AX078308 AX078308 8933 bp RNA linear PAT 22-FEB-2001
 LOCUS DEFINITION Sequence 4 from Patent WO0107661.
 ACCESSION AX078308
 VERSION AX078308.1 GI:13157999
 KEYWORDS SOURCE Synthetic construct
 ORGANISM Artificial sequences.
 FEATURES Location/Qualifiers 1_ .8933
 /organism="Synthetic construct"
 /mol type="unassigned RNA"
 /db xref="taxon:12630"
 /note="Sequence of the IAC-Asrc pseudo target"

variation	4135 . .4155 /note="Mutated positions: 4135, 4140-1, 4145, 4150, 4152-3, 4155"	ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 9748)
ORIGIN	Query Match Best Local Similarity 100.0%; Pred. No. 3.7e-28; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	REFERENCE	1 Nanshi, T.C. CLONING AND DEVELOPPING OF HTLV-III DNA PATENT: JP 1987026300-A 1 04-FEB-1987; SENTOKO INC
Qy	1 TTATTCATAATGATAGTAGTGGAGGCTTAAGATAAGATAATGGTTCTGTGACTTCT 60	COMMENT	OS human (homo sapiens) PN JP 1987026300-A/1 PD 04-FEB-1987 PF 11-OCT-1985 JP 1985226658 PR 10-OCT-1984 US 84 659339, 23-JAN-1985 US 85 693866 PI NANSHI TBII CHIYAN PC C07K3/00, A61K39/21, A61K39/35, C07R15/12, C12N5/00, C12N15/00, C12Q1/68, G01N33/574, G01N33/577; CC strandedness: Double; topology: Linear; hypoethical: No; PH Key PH Location/Qualifiers
Db	7630 TTATTCATAATGATAGTAGTGGAGGCTTAAGATAAGATAATGGTTCTGTGACTTCT 7689	FT 5'UTR FT promoter mat_Peptide	1 . .786 5'UTR product='gag p17 peptide' 787 . .1182 /product='gag p17 peptide' FT mat_Peptide FT gene=gag p17, >1185 /product='gag p24 peptide' FT mat_Peptide FT gene=gag p24, <2319 . .2322 /product='gag p15 peptide' FT mat_Peptide FT gene=gag p15, >2082 . .5126 /product='pol peptide' FT mat_Peptide FT gene=P1 FT mat_Peptide FT product='sor peptide' FT gene=sor, /product='sor peptide' FT intron FT mat_Peptide FT gene= P1 FT mat_Peptide FT 3'UTR FT 3'UTR Location/Qualifiers
RESULT 13	AX078313	FEATURES	1 . .9748 Source /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606"
LOCUS	AX078313	ORIGIN	Query Match Best Local Similarity 100.0%; Pred. No. 3.7e-28; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DEFINITION	Sequence 9 from Patent WO0107661.	Qy	1 TTATTCATAATGATAGTAGTGGAGGCTTAAGATAAGATAATGGTTCTGTGACTTCT 60 Best Local Similarity 100.0%; Pred. No. 3.7e-28; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	AX078313	Db	7630 TTATTCATAATGATAGTAGTGGAGGCTTAAGATAAGATAATGGTTCTGTGACTTCT 7689 /db_xref="taxon:32610" /note="Sequence of the IAC-Bscr pseudo target"
VERSION	GI:13158004	Qy	61 GTAGTGAATAGAGTTAGCAGGATATTCAACATTATCGTTTCAGCCACCTCCAAATC 120 /note="Sequence of the IAC-Bscr pseudo target"
KEYWORDS	Synthetic construct	Db	7690 GTAGTGAATAGAGTTAGCAGGATATTCAACATTATCGTTTCAGCCACCTCCAAATC 7749 /note="Sequence of the IAC-Bscr pseudo target"
SOURCE	Synthetic construct	Qy	121 CGGAGGGAA 129 /note="Mutated positions: 4140-42, 4145-47, 4152, 4156-57, 4159"
ORGANISM	artificial sequences.	Db	7750 CGGAGGGAA 7758 /note="Mutated positions: 4135, 4140-1, 4145, 4150, 4152-3, 4155"
REFERENCE	1 Numomura,K. Polymerase chain reaction method Patent: WO 0107661-A 9 01-FEB-2001; Gen-Probe Incorporated (US)	FEATURES	Source /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606"
AUTHORS		ORIGIN	Query Match Best Local Similarity 100.0%; Pred. No. 3.7e-28; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
TITLE		Qy	1 TTATTCATAATGATAGTAGTGGAGGCTTAAGATAAGATAATGGTTCTGTGACTTCT 60 Best Local Similarity 100.0%; Pred. No. 3.7e-28; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
JOURNAL		Db	8303 TTATTCATAATGATAGTAGTGGAGGCTTAAGATAAGATAATGGTTCTGTGACTTCT 832 /note="Sequence of the IAC-Bscr pseudo target"
FEATURES	1 . .9748 Source /organism="Homo sapiens" /mol type="genomic DNA" /db_xref="taxon:9606"	Qy	61 GTAGTGAATAGAGTTAGCAGGATATTCAACATTATCGTTTCAGCCACCTCCAAATC 120 /note="Sequence of the IAC-Bscr pseudo target"
SOURCE		Db	8363 GTAGTGAATAGAGTTAGCAGGATATTCAACATTATCGTTTCAGCCACCTCCAAATC 8422 /note="Sequence of the IAC-Bscr pseudo target"
variation		Qy	121 CGGAGGGAA 129 /note="Mutated positions: 4135, 4140-1, 4145, 4150, 4152-3, 4155"
ORIGIN	Query Match Best Local Similarity 100.0%; Pred. No. 3.7e-28; Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db	8423 CGGAGGGAA 8431 /note="Mutated positions: 4135, 4140-1, 4145, 4150, 4152-3, 4155"
RESULT 14	E01099	RESULT 15	REHTLV3 Human T-cell leukaemia type III (HTLV-III) proviral genome (AIDS virus for acquired immune deficiency syndrome).
LOCUS	E01099	REHTLV3	9748 bp RNA linear
DEFINITION	E01099	LOCUS	VRL 12-JUL-1999
ACCESSION	E01099.1	DEFINITION	Human T-cell leukaemia type III (HTLV-III) proviral genome (AIDS virus for acquired immune deficiency syndrome).
VERSION	GI:2169358		
KEYWORDS	Db		
SOURCE	Homo sapiens (human)		

X01762	GI:61569	2081.	'5125
ACCESSION	acquired immune deficiency syndrome; direct repeat; endonuclease;	/note="pol precursor polypeptides put. protease at 5' terminus" reverse transcriptase put. endonuclease at 3'	
WORDS	glycoprotein; inverted repeat; protease; provirus; reverse transcriptase; terminal repeat.	repeat_region 2128. .2163	
DEFINITION	Human immunodeficiency virus 1 (HIV-1)	/note="direct repeat"	
ORGANISM	Human immunodeficiency virus 1	repeat_region 2164. .2176	
AUTHORS	Lautenberger, J.A., Pearson, M.L., Petrucci, S.R.Jr., Ivanoff, I.I., Baumeister, K., Whitehorn, E.A., Rafalski, J.A., Doran, B.R., Josephs, S.J., Starcich, B., Livak, K.J., Patarca, R., Hasseltine, W.A. and Ratner, L.	/note="direct repeat"	
JOURNAL	Complete nucleotide sequence of the AIDS virus, HTLV-III	mRNA 5040. .5648	
MATERIALS	Nature 313 (6000), 277-284 (1985)	/note="SOR short open reading frame put. vestigial env gene"	
PUBLISHER	2578615	CDSS 6323. .8824	
PEER REVIEWED		/note="unnamed protein product; envelope glycoprotein"	
EXPERIMENTAL		repeate_start=1	
EXPERIMENTER		protein_id="CAA25903.1"	
EXPERIMENTAL		codon_start=1	
EXPERIMENTAL		db_xref="GI:61574"	
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EXPERIMENTAL		db_xref="SWISS-PROT:P03376"	
EXPERIMENTAL		/translation="MILMICSAITERKLWVYVYGPWKEATTFLCASDAKAYDTEVHN	
EXPERIMENTAL		WATHACYPDIDNPOEVVLVNNTENPNMMNDMEQEMDPLWSDQSLKPCVYLTLPL	
EXPERIMENTAL		CVSLKCDLKDNDTNTSSGGMIMERMEKPTNSPISITSRKGKVEYAFYKLDLIP	
EXPERIMENTAL		IDNDTSVLTSGNTSVLTAQCKVSFEPPIPHYCAPAGFAILKCNNKTFNGTGPCIN	
EXPERIMENTAL		VSTVOQTCGHIPVPUVPSVTOOLLNESSLEEVVIAVISANTFDKACTIIVOLNQSN	
EXPERIMENTAL		NNNTTRKSRIRIOPGPGRAPHFTIGKGNMRECGKNNLRECGNNK	
EXPERIMENTAL		TIIFKQSGGDEPVIFNSCQGBFFCNSTQFLNSTWNSITSTKGNTNTBESDTIT	
EXPERIMENTAL		DMRDNNRSELYKVKVVKLPGVAPTAKKRVRVRECRAGVGALEFGFGLAGSTMG	
EXPERIMENTAL		LPCRIKQIINNQEWGRAMYAPISQQRCSNTGILLTRDGNSBEIRPGGG	
EXPERIMENTAL		AASMTLTVQAROLLSGIVQQNNLRLAIEAQHLLQLT	
EXPERIMENTAL		EQSGLGWGSGLICLTPAQNNSLSLEQWNNTMENDREINNTSLIHSLKD	
EXPERIMENTAL		ESQNOQKNEOPLELDKWAISUNWNWNTNWYIKLFLMIVGGLGURIVFAYLSVV	
EXPERIMENTAL		NEVROQYSPLSPOTHPIPIRGFDRPEGIEEGERDDRRDSTILVNGSLAIIDDLRSL	
EXPERIMENTAL		CLFSYHLRDLJLIVTGVATRNLQYWSQELKNSAVSLNATA	
EXPERIMENTAL		VAEGTDRVYVQGAYRAIRHPPRLRQGLERILL"	
EXPERIMENTAL		misc_feature 7786. .7787	
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EXPERIMENTAL		mRNA 7787. .8821	
EXPERIMENTAL		/note="put. lor transmembrane protein"	
EXPERIMENTAL		9098. .9103	
EXPERIMENTAL		/note="poly purine stretch"	
EXPERIMENTAL		9115. .9748	
EXPERIMENTAL		/note="long terminal repeat"	
EXPERIMENTAL		9115. .9567	
EXPERIMENTAL		/note="U3 region"	
EXPERIMENTAL		9558. .9665	
EXPERIMENTAL		/note="R region"	
EXPERIMENTAL		9641. .9646	
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EXPERIMENTAL		9666. .9748	
EXPERIMENTAL		/note="U5 region"	
EXPERIMENTAL		9747. .9748	
EXPERIMENTAL		/note="inverted repeat"	
EXPERIMENTAL		ORIGIN	
EXPERIMENTAL		Query Match 100.0%	
EXPERIMENTAL		Best Local Similarity 100.0%	
EXPERIMENTAL		Pred. No. 3.7e-28;	
EXPERIMENTAL		Mismatches 0;	
EXPERIMENTAL		Indels 0;	
EXPERIMENTAL		Gaps 0;	
EXPERIMENTAL		Db 8303 TTATTCATATGATAGTAGGTAGGGTTAGATAGTGTCTGTTCTCTCTCT	
EXPERIMENTAL		Qy 1 TTATTCATATGATAGTAGGTAGGGTTAGATAGTGTCTGTTCTCTCTCT	
EXPERIMENTAL		Db 8303 TTATTCATATGATAGTAGGTAGGGTTAGATAGTGTCTGTTCTCTCT	
EXPERIMENTAL		Qy 61 GTACTGAATAGATAGGTAGGGTTAGATAGTAGGTAGGGTTAGATAGTGTCTGTTCT	
EXPERIMENTAL		Db 8303 TTATTCATATGATAGTAGGTAGGGTTAGATAGTGTCTGTTCTCTCT	
EXPERIMENTAL		Qy 787. .1182.	
EXPERIMENTAL		/product=gag p17"	
EXPERIMENTAL		1183. .2321	
EXPERIMENTAL		/note="gag p24 and gag p15 for major capsid protein and	
EXPERIMENTAL		for put. retroviral nucleic acid binding protein	
EXPERIMENTAL		repeat_region 1968. .2002	
EXPERIMENTAL		/note="direct repeat"	
EXPERIMENTAL		repeat_region 2031. .2065	
EXPERIMENTAL		/note="direct repeat"	
EXPERIMENTAL		Db 8423 CCGAGGGAA 8431	

PAGINATIONS

RESULT	1
LOCUS	AB036462/c
DEFINITION	Mus musculus CDNA clone 13-3, mRNA sequence.
ACCESSION	AB036462
VERSION	AB036462.1
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
MATERIAL	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
KEYWORDS	Euteleostomi;
REFERENCE	Wang, Y.I., Saigo, H., Osaka, H., Yamamichi, T., Suh, J.G., Kiyosawa, H., Sakai, Y., Watanabe, S., and Wada, Y.
AUTHORS	(bases 1 to 317)

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

IMMATURE

Result	No.	Score	Query	Match	Length	DB	ID	Description	
								%	Start
1	1	90	100.0	317	9	AB034462		AB034462	AB034462
	2	88.4	98.2	527	28	BH886550		BH886550	BH008651a.
	3	34	37.8	809	29	CG67892		CG67892	ZMBBC016
	4	34	37.8	925	29	CC74059		CC74059	OGUBBX71TV

FEATURES clones (437N8, 538Q24, Research Genetics) using exon trapping method.
 source Location/Qualifiers
 1_317 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129/Sv"
 /db_xref="taxon:10090"
 /map="5"
 /clone="13-3"
 /sex="male"
 /tissue_type="brain,liver,kidney,lung,heart,spleen"
 /cell_line="CJ7 embryonic stem cell line"
 /dev_stage="adult"
 /clone_lib="Mus musculus CJ7 brain, liver, kidney, lung, heart, spleen"

ORIGIN

Query Match 100.0%; Score 90; DB 9; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAGATGAGGAGAAATATCAGACTCTGGGATGGGGTGAATGGGGACCATG 60
 Db 141 ATGAGATGAGGAGAAATCAGACCTGTGGACATGGGGTGAATGGGGACCATG 82
 Qy 61 CTCCCTGGATGTTGATGATCTGTAGTCT 90
 Db 81 CTCCCTGGATGTTGATGATCTGTAGTCT 52

RESULT 2

BH886550/c LOCUS BH886550 527 bp DNA linear GSS 07-AUG-2002
 DEFINITION Leishmania major Friedlin BAC Library Leishmania
 major genomic clone LB00861a, genomic survey sequence.

COMMENT

TITLE

JOURNAL

AUTHORS

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

JOURNAL

COMMENT

FEATURES

source

Location/Qualifiers

1_527

/organism="Leishmania major"

/mol_type="Genomic DNA"

/strain="Friedlin"

/db_xref="taxon:5664"

/clone_id="B00861a"

/lab_host="E. coli GeneHogs + TrfA"

/clone_lib="Leishmania major Friedlin BAC Library"

/note="Vector: pCC270; Site: 1; HindIII; Genomic DNA from

Leishmania major Friedlin in agarose blocks was partially

digested with HindIII, size selected, and ligated with

HindIII-digested PCG2/0 vector DNA. 10368 clones were

picked and arrayed in 384- and 96-well plates. Library

construction and arraying was carried out by ResGen

Corporation and clones and filters are available from

RESULTS

4

CC714059

FEATURES clones (437N8, 538Q24, Research Genetics) using exon trapping method.
 source Location/Qualifiers
 1_317 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="129/Sv"
 /db_xref="taxon:10090"
 /map="5"
 /clone="13-3"
 /sex="male"
 /tissue_type="brain,liver,kidney,lung,heart,spleen"
 /cell_line="CJ7 embryonic stem cell line"
 /dev_stage="adult"
 /clone_lib="Mus musculus CJ7 brain, liver, kidney, lung, heart, spleen"

ORIGIN

Query Match 100.0%; Score 90; DB 9; Length 317;
 Best Local Similarity 100.0%; Pred. No. 1.4e-14;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 ATGAGATGAGGAGAAATATCAGACTCTGGGATGGGGTGAATGGGGACCATG 60
 Db 141 ATGAGATGAGGAGAAATCAGACCTGTGGACATGGGGTGAATGGGGACCATG 82
 Qy 61 CTCCCTGGATGTTGATGATCTGTAGTCT 90
 Db 81 CTCCCTGGATGTTGATGATCTGTAGTCT 52

RESULT 3

CG687892 LOCUS CG687892 809 bp DNA linear GSS 08-OCT-2003
 DEFINITION ZMMBBC0165122r ZMMBBC (EcORI) Zea mays genomic clone
 ZMMBBC0165122 3', genomic survey sequence.

DEFINITION

ACCESSION CG687892

KEYWORDS GSS.

SOURCE Zea mays subsp. mays (maize)

ORGANISM Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:

Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae; PACCAD

CLADE: Panicoideae; Zea.

REFERENCE 1 (bases 1 to 809)

AUTHORS Bharti, A.K., Young, S., Kavchik, S., Keiser, G., Bronzino, A.C.,
 Zohrehzad, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.

COMMENT Unpublished (2003)

TITLE Sequencing of the maize genome at PGIR (2003c)

JOURNAL Unpublished (2003)

CONTACT Bharti, A.K.

Dr. Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers

University

190 Frelinghuysen Road, Piscataway, NJ 08854, USA

Tel: 732 445 3801

Fax: 732 445 5735

Email: bharti@waksman.rutgers.edu

Seq primer: SP6

Class: BAC ends

High quality sequence start: 400.

LOCATION/QUALIFIERS

1_809

/organism="Zea mays subsp. mays"

/mol_type="Genomic DNA"

/cultivar="73"

/sub_species="mays"

/db_xref="Taxon:4578"

/clone_id="ZMMBBC0165122"

/lab_host="E. coli DH10B"

/clone_lib="ZMMBBC (EcORI)"

/note="vector: PTARBAC2.1; site_1: EcoRI; site_2: EcoRI"

ORIGIN

Query Match 37.8%; Score 34; DB 29; Length 809;
 Best Local Similarity 63.4%; Pred. No. 50;
 Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

Qy 2 TGAGATGTTGATGATGATCTG 83

Db 575 TGAGATGTTGATGATGATCTG 65

Qy 62 TCCCTGGATGTTGATGATCTG 83

Db 635 TGCTGGTGGCTCATCTG 65

LOCUS CG714059 925 bp DNA linear GSS 19-JUN-2003
 DEFINITION genomic survey sequence.
 ACCESSION CG714059
 VERSION GSS.
 KEYWORDS Zea mays
 SOURCE Organism
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade; Panicoidea; Andropogoneae; Zea.
 1. (bases 1 to 925)
 REFERENCE Whitehead C.A., Quackenbush J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nunberg, A., Robbins, D., and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2003)
 Other GSS: OGBBX71TH
 Contact: Cathy Whitelaw
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-8243
 Fax: 301-838-0208
 Email: whitelaw@tigr.org
 Seq. Primer: TF
 Class: sheared ends.
 Location/Qualifiers 1..925
 /organism="Zea mays"
 /mol_type="Genomic DNA"
 /strain="M73"
 /db_xref="taxon:4577"
 /clone="ZMMBMa0404K22"
 /clone_lib="ZM 0.7-1.5 KB"
 /note="Vector: PBCSK-5 Site 1; HincII; 0.7-1.5 kb
 methylation filtered genomic DNA library"
 FEATURES source
 Query Match 37.8%; Score 34; DB 29; Length 925;
 Best Local Similarity 63.4%; Pred. No. 53;
 Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Qy 2 TGAGTGAAAGGAGAAATACTGGACTGTGGAGATGGGGCACCATGC 61
 Db 342 TGAGTCATGAGAACTCGCTCATGTCATGGTGGTGTGGAGCACTGC 401
 ORIGIN
 Query Match 37.8%; Score 34; DB 29; Length 925;
 Best Local Similarity 63.4%; Pred. No. 53;
 Matches 52; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Qy 2 TGAGTGAAAGGAGAAATACTGGACTGTGGAGATGGGGCACCATGC 61
 Db 342 TGAGTCATGAGAACTCGCTCATGTCATGGTGGTGTGGAGCACTGC 401
 Qy 62 TCCCTGGATGTGTGATGATCTG 83
 Db 402 TCTGGGGCTCATGTTG 423
 RESULT 5
 LOCUS CD850313 473 bp mRNA linear EST 11-JUL-2003
 DEFINITION DH0AC3BZ11RM1 HaDevR2 Helianthus annuus cDNA clone HaDevR238A11,
 mRNA sequence.
 ACCESSION CD850313
 VERSION CD850313_1 GI:325254135
 KEYWORDS EST.
 SOURCE Helianthus annuus (common sunflower)
 Helianthus annuus
 ORIGIN
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; Campanulids; Asterales; Asteraceae; Asteroideae;
 Helianthaceae; Helianthus.
 Helianthaceae
 Genoplante, a major partnership french program in plant genomics
 Unpublished (2003)
 Contact: Genoplante
 Genoplante
 93, rue Henri Rochefort 91025 EVRY CEDEX France
 Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10
 This sequence has been generated in the framework of the french
 plant genomics programme "Genoplante" (<http://www.genoplante.com>
 and <http://genoplante-info.infobioingen.fr>).
 Location/Qualifiers
 1..473
 /organism="Helianthus annuus"
 /mol_type="mRNA"
 /cultivar="HaDevR2"
 /db_xref="taxon:42422"
 /clone="HaDevR238A11"
 /tissue_type="terminal bud"
 /clone_1Ib="HaDevR2"
 ORIGIN
 Query Match 36.2%; Score 32.6; DB 14; Length 473;
 Best Local Similarity 60.9%; Pred. No. 99;
 Matches 53; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
 Qy 1 ATGAGAGTGAAGGAGAAATACTGGACTGTGGAGATGGGGCACCATG 60
 Db 291 AGGACATGGGCAACTACTAACATTGAGATGGAGGAGGAGGAGGAGAAG 350
 Qy 61 CTCCCTGGATGTGTGATCTGTACT 87
 Db 351 CTGCTGGTGAACCATGTGTACT 377
 RESULT 6
 CD230371/c
 LOCUS SS1_43_D04_b1_A012_Salt-stressed seedlings Sorghum bicolor cDNA
 DEFINITION clone_SS1_43_D04_A012_3, mRNA sequence.
 ACCESSION CD230371_1
 VERSION GI:30973805
 KEYWORDS EST.
 SOURCE Sorghum bicolor (Sorghum)
 ORGANISM Sorghum bicolor
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyra; Liliopsida; Poales; Poaceae; PACCD
 Clade; Panicoidea; Andropogoneae; Sorghum.
 1 (bases 1 to 454)
 REFERENCE Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
 Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Summer,E.J.,
 Eastman,A., and Pratt,L.H.
 AUTHORS Unpublished (2003)
 TITLE Other_Etis: SS1_43_D04_91_A012
 JOURNAL COMMENT Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: impratt@uga.edu
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in
 the Human Genome Center, University of Tokyo Institute of Medical
 Science, Plant material and RNA prepared at Texas A & M University;
 sequencing done in the Laboratory for Genomics and Bioinformatics,
 University of Georgia. Sequence ends have been trimmed to exclude
 vector and regions below Phred quality 16. Three-prime sequences
 are presented as their reverse complement and have been trimmed to
 exclude polyA.
 Seq primer: Sug3 (CGACCTGGCTGGCTGAGCACA)
 POLYA=1e⁸.
 FEATURES source
 /organism="Sorghum bicolor"
 /mol_type="mRNA"
 /cultivar="SS1_43_D04_91_A012"
 /db_xref="taxon:4558"
 /clone="SS1_43_D04_91_A012"
 /lab_host="DH10B-T1 phage-resistant E. coli"

/clone.lib="Salt-stressed seedlings"
 /note="Vector: pME18S-FRL3; Site_1: XbaI; Site_2: XbaI; The library was prepared from a mixture of polyA+ RNA from callus culture tissue and cells in suspension culture. Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FRL3 vector (5'-prime DraIII site is CACTGTCG, 3'-prime DraIII site is CACCATGG). XbaI excises the cDNA insert."
 Double-stranded cDNA was cloned unidirectionally into different DraIII sites of the pME18S-FRL3 vector (5'-prime DraIII site is CACTGTCG, 3'-prime DraIII site is CACCATGG)."

ORIGIN

Query Match 35.6%; Score 32; DB 14; Length 515;
 Best Local Similarity 68.8%; Pred. No. 1.4e+02;
 Matches 44; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Qy 23 AGCACTTGGAGATGGGGATGGAGATGGGGCACCATGGCTGGATTTGATGATC 82
 Db 97 AGGGTTGGAGATCTGGAGATCTGGAGATTGGATTTGATGGATGTT 38
 Qy 83 GTAG 86
 Db 100 GGAG 97

RESULT 8
 CG172989 LOCUS CG172989 94 bp DNA linear GSS 21-AUG-2003
 DEFINITION PUPPC46TD ZM_0_6_1.0_KB Zea mays genomic clone ZMMBta0701G19,
 Db 160 AGAGGTTGGAGATGGGGCACCATGGCTGGATTTGATGGATTT 101

ORIGIN

Query Match 35.6%; Score 32; DB 14; Length 515;
 Best Local Similarity 68.8%; Pred. No. 1.4e+02;
 Matches 44; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Qy 23 AGCACTTGGAGATGGGGATGGAGATGGGGCACCATGGCTGGATTTGATGATC 82
 Db 97 AGGGTTGGAGATCTGGAGATCTGGAGATTGGATTTGATGGATGTT 38
 Qy 83 GTAG 86
 Db 100 GGAG 97

RESULT 8
 CG172989 LOCUS CG172989 94 bp DNA linear GSS 21-AUG-2003
 DEFINITION PUPPC46TD ZM_0_6_1.0_KB Zea mays genomic clone ZMMBta0701G19,
 Db 160 AGAGGTTGGAGATGGGGCACCATGGCTGGATTTGATGGATTT 101

ACCESSION CG172989
 VERSION CG172989.1 GI:34063787
 KEYWORDS
 SOURCE zeamay
 ORGANISM zeamay
 Eukaryota; Viridiplantae; Streptophytida; Embryophytida; Tracheophytida; Spermatophytida; Magnoliophytida; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidea; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 94)
 AUTHORS Whitehead,C.A.; Quackenbush,J.; Van Aken,S.; Utterback,T.; Bennetzen,J.
 COMMENT Unpublished (2003)
 Other GSS: PURPC46TB
 Contact: Cathy Whitehead
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-338-5843
 Fax: 301-338-0208
 Email: whitehead@tigr.org
 Seq Primers: TF
 Class: sheared ends
 FEATURES Location/Qualifiers
 source 1..940
 /organism="Zea mays"
 /mol_type="genomic DNA"
 /strain="B73"
 /db_xref="Taxon:4577"
 /clone="ZMMBta0701G19"
 /clone.lib="ZM_0_6_1.0_KB"
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
 Cot selected genomic DNA library"

ORIGIN

Query Match 34.4%; Score 31; DB 29; Length 940;
 Best Local Similarity 62.0%; Pred. No. 3.6e+02;
 Matches 49; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 Qy 8 TGAGGAGAAATACTGACATGTGGAGATGGGGACCATGCTCTTG 67
 Db 146 TGATCCATAGTCTGATGTTGGAGCTAGGGAGGTGGGGAAACCTGCTGTT 205
 Qy 68 GGATGTTGATGATGATGATGATGATG 86
 Db 206 TGCCCGTAGCAGGCTAG 224

FEATURES source
 Location/Qualifiers
 1..515
 /organism="Sorghum bicolor"
 /mol_type="DNA"
 /cultivar="IRIX430"
 /db_xref="Taxon:4558"
 /clone="ZCC1_66_C06_A007"
 /lab_host="DRI0B-T1 phage-resistant E. coli"
 /clone.lib="Callus culture/cell suspension"
 /note="Vector: pME18S-FRL3; Site_1: XbaI; Site_2: XbaI; The

RESULT 9 CA485128/c LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	CA485128 WHE4314_G11_M22ZS Wheat meliotic anther cDNA library EST 14-NOV-2002 mRNA mRNA clone WHE4314_G11_M22, mRNA sequence.	634 bp linear EST 14-NOV-2002	nw85d06.81 NCI-CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253387 similar to contains element MER28 repetitive element ; mRNA sequence. AA879214 AA879214.1 GI:2988179 EST. Homo sapiens (human)
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R., Pham, J., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.	Triticum aestivum (bread wheat) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.	nw85d06.81 NCI-CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253387 similar to contains element MER28 repetitive element ; mRNA sequence. AA879214 AA879214.1 GI:2988179 EST. Homo sapiens (human)
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R., Pham, J., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.	Triticum aestivum (bread wheat) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.	nw85d06.81 NCI-CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253387 similar to contains element MER28 repetitive element ; mRNA sequence. AA879214 AA879214.1 GI:2988179 EST. Homo sapiens (human)
REFERENCE AUTHORS TITLE JOURNAL COMMENT	Anderson, O.D., Chao, S., Crossman, C., Langridge, P., Lazo, G.R., Pham, J., Rausch, C.J., Sutton, T., Woo, J. and Wilson, C.	Triticum aestivum (bread wheat) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.	nw85d06.81 NCI-CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253387 similar to contains element MER28 repetitive element ; mRNA sequence. AA879214 AA879214.1 GI:2988179 EST. Homo sapiens (human)
FEATURES source	1 - 634 /organism="Triticum aestivum" /mol_type="mRNA" /cultivar="Chinese Spring" /db_xref="taxon:4565" /clone="WHE4314_G11_M22" /tissue_type="Anther" /dev_stage="Meiotic stages pre-meiosis-metaphase I" /lab_host="E. coli DH10B" /clone_lib="wheat meiotic anther cDNA library" /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; Plants were grown in a glasshouse. Anther meiotic stage was determined by removing anthers from individual primary florets. One anther was sacrificed for microscopic staging, and if determined to be between (and including) meiotic stages pre-meiosis and metaphase I, the remaining two anthers were collected and pooled for library construction. The tissue, total RNA, and poly(A) RNA were prepared, cDNA synthesised, and directionally ligated into pSPORT1 by Tim Sutton in the P Langridge Lab at the Department of Plant Science, University of Adelaide, Waite Campus, Australia. Average insert size 1.5kb. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."	Query Match Best Local Similarity 34.0%; Score 30.6; DB 14; Length 634; Matches 51; Conservative 0; Mismatches 34; Indels 0; Gaps 0; QY 1 ATGAGATGAGGAAATACTGGACTTGAGATGGGGGTGAGATGGGCACCATG 60 Db 209 ATGGAGAAAGAGGAGAACCCGAGCACTAGAAGGGCAGGAGTGAAGC 150 QY 61 CTCCCTGGATGGATGTCGATCTGTGTA 85 Db 149 GTCCCTGGATGGATGAAGAGGTA 125	nw85d06.81 NCI-CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253387 similar to contains element MER28 repetitive element ; mRNA sequence. AA879214 AA879214.1 GI:2988179 EST. Homo sapiens (human)
RESULT 10 AAB9214/c LOCUS	CA485128.1 EST.	225 bp mRNA linear EST 25-MAR-1998	nw85d06.81 NCI-CGAP_Pr12 Homo sapiens cDNA clone IMAGE:1253387 similar to contains element MER28 repetitive element ; mRNA sequence. AA879214 AA879214.1 GI:2988179 EST. Homo sapiens (human)

JOURNAL	Unpublished (1997)	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
cdNA Library Preparation:	M. Bento Soares, Ph.D.	cdNA Library Preparation:	M. Bento Soares, Ph.D.
cdNA Library Arrayed by:	Greg Lennon, Ph.D.	cdNA Library Arrayed by:	Greg Lennon, Ph.D.
cdNA Sequencing by:	Washington University Genome Sequencing Center	cdNA Sequencing by:	Washington University Genome Sequencing Center
Clone distribution by:	Washington University Genome Sequencing Center	Clone distribution by:	Washington University Genome Sequencing Center
found through the I.M.A.G.E. Consortium/LJNL at:	www-bio.ljnl.gov/bbrp/image/image.html	found through the I.M.A.G.E. Consortium/LJNL at:	www-bio.ljnl.gov/bbrp/image/image.html
Insert Length:	1762 Std Error: 0.00	Insert Length:	1155 Std Error: 0.00
Seq primer:	-40ml3 fwd. ET from Amersham	Seq primer:	-40ml3 fwd. ET from Amersham
High quality sequence stop:	167.	High quality sequence stop:	164.
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	1.. 274		/organism="Homo sapiens" /mol_type="mRNA" /db_xref="LXON-9606" /clone="IMAGB:1517882" /tissue type="pooled germ cell tumors" /lab_host="DH10B" /clone_lib="NCI_GAP GC4" /note="vector: pTT3D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from 3 pooled germ cell tumors, and was then primed with a Not I - oligo(dN) primer. Double-stranded cDNA was digested with Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "
FEATURES	Location/Qualifiers	Source	
	1.. 274		Query Match Score 30.2; DB 9; Length 294; Best Local Similarity 60.2%; Pred. No. 3.7e+02; Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
FEATURES	Location/Qualifiers	Source	
	1.. 274		Query Match Score 30.2; DB 9; Length 294; Best Local Similarity 60.2%; Pred. No. 3.7e+02; Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
ORIGIN			
			Query Match Score 30.2; DB 9; Length 294; Best Local Similarity 60.2%; Pred. No. 3.7e+02; Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
ORIGIN			Query Match Score 30.2; DB 9; Length 294; Best Local Similarity 60.2%; Pred. No. 3.7e+02; Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
ORIGIN			Query Match Score 30.2; DB 9; Length 294; Best Local Similarity 60.2%; Pred. No. 3.7e+02; Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
ORIGIN			Query Match Score 30.2; DB 9; Length 294; Best Local Similarity 60.2%; Pred. No. 3.7e+02; Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
RESULT 13			Query Match Score 30.2; DB 9; Length 294; Best Local Similarity 60.2%; Pred. No. 3.7e+02; Matches 50; Conservative 0; Mismatches 33; Indels 0; Gaps 0;
LOCUS	AA932668	DEFINITION	AA932668 NCBI CGAP GC4 Homo sapiens cDNA clone IMAGE:1571882 3'
DEFINITION	AA932668	DEFINITION	similar to contains_element MER28 repetitive element ; mRNA sequence.
ACCESSION	AA932668	VERSION	AA932668.1 GI:30866333
KEYWORDS		EST.	
SOURCE	Homo sapiens	ORGANISM	Homo sapiens (human)
ORGANISM		REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. (bases 1 to 301)
REFERENCE		AUTHORS	Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Dias Neto, B., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
COMMENT		DEFINITION	Nagai, M.A., da Silva, W.Jr., Zago, M.A., Bordim, S., Costa, F.F., Goldmann, G.H., Carvalho, A.P., Matsukuma, A., Bajia, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F.R., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
COMMENT		VERSION	GI:14390801
COMMENT		KEYWORDS	shotgun sequencing of the human transcriptome with ORF expressed sequence tags
COMMENT		TITLE	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT		JOURNAL	JOURNAL MEDLINE
COMMENT		PUBLMED	20202663
COMMENT		COMMENT	10737800 Contact: Simpson A.J.G.
COMMENT		COMMENT	Laboratory of Cancer Genetics Ludwig Institute for Cancer Research
COMMENT		COMMENT	Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br

Page 7

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. It can be seen in the following URL
<http://www.ludwig.org/bi/scripts/gethtml2.pl?cl=MR1&t2=MR1-HTM183-0101-002-a06&t3=2001-01-04&t4=1>

Q primer: puc 18 forward
 Q quality sequence start: 24
 Q quality sequence stop: 301.

Location/Qualifiers

1. .301

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_id="HTM183"
/clone_start="Adult"
/clone_end="Head neck; vector: puc18; Site 1: Smal;
/note="Organ: head/neck; vector: puc18; Site 1: Smal;
Site 2: Small; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent Application
No. 196,716 - Ludwig Institute for Cancer Research)
Profiles into the PUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

```

ORIGIN	Quer	RESULT	ACCESS
Best	Best	AW7892	VERSION
Match	Match	LOCUS	KEYWORD
		DEFINI	SOURCE
	QY		
	Db		

ORGANISM	REFERENCE AUTHORITY	TITLE	JOURNAL	COMMENT
similarity 33.6%; Conservative 60.2%; ; Pred. No. 3.8e+02; 0; Mismatches 33;	Score 30.2; Length 301; DB 12; REFREP; AUTH	Indels 0; Gaps 0;	ATAGAGTGAACGAGAATAATAGCACTTGTGGAGATGGGTGCGAATGGGCACATG AAAAGGAGGAGGAACTGCACAGATGAGGAAGAGGAGGAGGAATG CTCTCTGGATGTTGATGATCNG B3 ATATGATGATGATGATGATGTC 4.9	

788422 386 bp mRNA linear EST 01-MAY-2001
0-35-F Lambda Zap, Stratagene Blumeia graminis f. sp. hordei
clone C00435 similar to adenylyl cyclase-associated protein 2
cDNA

NA sequence.
788422 GI:13900019
788422.1 GI:13900019
T.
Thlaspium graminis f. sp. *hordei*
Thlaspium graminis f. sp. *hordei*
Kakuro. Funct. Ascromyces. Deszumocytina. Testicomyces.

Search
Job title

all: sw@crc.dk
 Eh quality sequence stop: 386
 LYA=No.

Location/Qualifiers	1.
	.386
	/organism="Blumeria graminis f. sp. hordei"
	/mol_type="mRNA"
	/db_xref="Axon:62688"
	/clone="C00435"
	/cell_type="conidia"
	/lab_host="Hordeum vulgare"
	/conditile="condidium"
	/conditile_id="condidium_1"

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw mode
Run on: March 11, 2004, 18:52:43 ; Search time 675.083 Seconds
(without alignments)
6934.037 Million cell updates/sec

Title: US-10-003-035-25
Perfect score: 108
Sequence: 1 tgtaaaagcccaataacaacaa.....atatggagaacaaaggcacatgt 108

Scoring table: IDENTITY_NUC
Gapop 1.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
 1: gb_ba:
 2: gb_htg:
 3: gb_in:
 4: gb_om:
 5: gb_ov:
 6: gb_dat:
 7: gb_ph:
 8: gb_pl:
 9: gb_pr:
 10: gb_ro:
 11: gb_stb:
 12: gb_sy:
 13: gb_un:
 14: gb_vl:
 15: em_ba:
 16: em_fum:
 17: em_hum:
 18: em_in:
 19: em_mu:
 20: em_om:
 21: em_or:
 22: em_ov:
 23: em_pat:
 24: em_ph:
 25: em_pl:
 26: em_rc:
 27: em_stb:
 28: em_un:
 29: em_vl:
 30: em_htg_hum:
 31: em_htg_inv:
 32: em_htg_other:
 33: em_htg_mus:
 34: em_htg_pln:
 35: em_htg_rod:
 36: em_htg_mam:
 37: em_htg_vrt:
 38: em_sy:
 39: em_htg_hum:
 40: em_htg_mus:
 41: em_htg_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description				
1	108	100.0	AY289013	HIV-1 clade A				
2	108	100.0	M64190	Human immunodeficiency virus 1 (HIV-1)				
3	108	100.0	M61582	Human immunodeficiency virus 1 (HIV-1)				
4	108	100.0	M61584	Human immunodeficiency virus 1 (HIV-1)				
5	108	100.0	M61585	Human immunodeficiency virus 1 (HIV-1)				
6	108	100.0	M61586	Human immunodeficiency virus 1 (HIV-1)				
7	108	100.0	D78624	HIV-1 isolates				
8	108	100.0	M64768	Human immunodeficiency virus 1 (HIV-1)				
9	108	100.0	L48399	Human immunodeficiency virus 1 (HIV-1)				
10	108	100.0	105601	Sequence 7				
11	108	100.0	105603	Sequence 9				
12	108	100.0	U40538	Human immunodeficiency virus 1 (HIV-1)				
13	108	100.0	U40539	Human immunodeficiency virus 1 (HIV-1)				
14	108	100.0	105605	Sequence 11				
15	108	100.0	105295	Sequence 5				
16	108	100.0	106664	Sequence 6				
17	108	100.0	105360	Sequence 10				
18	108	100.0	105297	Sequence 6				
19	108	100.0	105665	Sequence 7				
20	108	100.0	106663	Sequence 5				
21	108	100.0	10588	Sequence 4				
22	108	100.0	106666	Sequence 8				
23	108	100.0	105298	Sequence 7				
24	108	100.0	105365	Sequence 13				
25	108	100.0	105361	Sequence 11				
26	108	100.0	105299	Sequence 8				
27	108	100.0	AR365081	Sequence 8				
28	108	100.0	M15654	Human immunodeficiency virus 1 (HIV-1)				
29	108	100.0	AR094659	Genomic DNA				
30	108	100.0	AR382018	Sequence 11				
31	108	100.0	X078307	Human T-cell				
32	108	100.0	AX078308	Sequence 1				
33	108	100.0	AX078313	Human immunodeficiency virus 1 (HIV-1)				
34	108	100.0	E009817	Genomic DNA				
35	108	100.0	I04549	Sequence 11				
36	108	100.0	E01099	DNA sequence				
37	108	100.0	K01762	Human T-cell				
38	108	100.0	I07983	Sequence 1				
39	108	100.0	AY078308	Human immunodeficiency virus 1 (HIV-1)				
40	107	99.1	M64773	Human immunodeficiency virus 1 (HIV-1)				
41	106.4	98.5	42	106.4	98.5	108	14	HIVLAAAB
42	106.4	98.5	43	106.4	98.5	108	14	HIVLAAC
43	106.4	98.5	44	106.4	98.5	108	14	HIVLAAH
44	106.4	98.5	45	106.4	98.5	108	14	HIVLAJ

ALIGNMENTS

RESULT 1	AY289013	AY289013	AY289013	108 bp DNA linear glycoprotein gene, partial cds.
LOCUS				
DEFINITION				
VERSION	AY289013.1	AY289013.1	AY289013.1	GI:32264045
KEYWORDS				
SOURCE				Human immunodeficiency virus 1 (HIV-1)
ORGANISM				Viruses; Retroviridae; Lentiviridae; Lentivirus; Primate lentivirus group.
REFERENCE	1 (bases 1 to 108)			
AUTHORS	Hoshino,Y., Tse,D.B., Prabhakar,S., Hoshino,S., Kuwabara,K., Ching,E., Raju,B., Gold,J.A., Borkowsky,W.N., Rom,W.N.,			

Pred. No. is the number of results predicted by chance to have a

TITLE Weiden, M., and Pine, R.
The Innate Immune Response to Tuberculosis Alters CXCR4 (CD184) and
Beta Chemokine Expression Enhancing HIV-1 X4 Strain Entry into
Alveolar Macrophages
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 108)
AUTHORS Yoshino, Y., Tse, D.B., Rochford, G., Prabhakar, S., Hoshino, S.,
Kuwabara, K., Ching, E., Raju, B., Gold, J.A., Borowsky, W., Rom, W.N.,
Weiden, M., and Pine, R.
DIRECT SUBMISSION
Submitted (01-MAY-2003) Medicine, New York University Medical
Center, 462 First Avenue NB 8E38, New York, NY 10016, USA
LOCATION/QUALIFIERS
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/organism="Human immunodeficiency virus 1"
/mol type="genomic DNA"
/isolation source="patient co-infected with tuberculosis;
from bronchoalveolar lavage fluid"
/db_xref="taxon:11676"
/clone="BAL21"
/country="USA"
/note="anti-CD14 antibody captured"
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/gene="env"
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/product="envelope glycoprotein"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.5e-20;
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/translation="CTRPNNNTRKSTRIQRGPGRAFVTIGKIGNMRQAHC"

TITLE
JOURNAL
FEATURES
SOURCE

Query Match 100.0% Score 108; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.5e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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TITLE
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SOURCE

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TITLE
JOURNAL
FEATURES
SOURCE

Query Match 100.0% Score 108; DB 14; Length 108;
Best Local Similarity 100.0%; Pred. No. 4.5e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

/organism="Human immunodeficiency virus 1"
/mol type="genomic DNA"
/isolation source="patient co-infected with tuberculosis;
from bronchoalveolar lavage fluid"
/db_xref="taxon:11676"
/clone="BAL21"
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/db_xref="GI:32261046"
/translation="CTRPNNNTRKSTRIQRGPGRAFVTIGKIGNMRQAHC"
ORIGIN

RESULT 3
HIVV3166
DEFINITION Human immunodeficiency virus type 1 (HIV-1) envelope gene V3
ACCESSION M61582
VERSION M61582_1 GI:485339
KEYWORDS
ORGANISM Human immunodeficiency virus 1 (HIV-1)
DEFINITION Human immunodeficiency virus 1
ACCESSION M61582
VERSION M61582_1 GI:485339
KEYWORDS envelope-associated protein
SOURCE
ORGANISM Human immunodeficiency virus 1
Viruses; Retroviridae; Lentiviridae; Lentivirus; Primate
DEFINITION
REFERENCES 1 (bases 1 to 108)
AUTHORS LaRosa, G.J., Davide, J.P., Weinhold, K., Waterbury, J.A., Proffy, A.T.,
Lewis, J.A., Langlois, A.J., Dresman, G.R., Boswell, R.N.,
Shadduck, P., Holley, L.H., Karplus, M., Bolognesi, D.P.,
Matthews, T.J., Emini, E.A., and Putney, S.D.
TITLE
JOURNAL Science 269 (1991), 932-935 (1990)
MEDLINE 239285
PUBMED
COMMENT Original source text: Human immunodeficiency virus type 1 V3 region
FEATURES
SOURCE
ORGANISM
DEFINITION Human immunodeficiency virus type 1 V3 region
ACCESSION M61582
VERSION M61582_1 GI:485339
KEYWORDS envelope-associated protein
SOURCE
ORGANISM Human immunodeficiency virus 1 (HIV-1)
Viruses; Retroviridae; Lentiviridae; Lentivirus; Primate
DEFINITION
REFERENCES 1 (sites)
AUTHORS Wain-Hobson, S., Vartanian, J.-P., Henry, M., Chenciner, N.,
Cheynier, R., Delessus, S., Martins, L.P., Sala, M., Nugeyre, M.-T.,
Gustard, D., Klatmann, D., Gluckman, J.-C., Rozenbaum, W.,
Barre-Sinoussi, F., and Montagnier, L.
TITLE
JOURNAL Science 252 (1991), 961-965 (1991)
MEDLINE 205026
PUBMED
COMMENT Original source text: Human immunodeficiency virus type 1 (HIV-1)
PROVIRAL DNA, clone C8
LOCATION/QUALIFIERS
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Best Local Similarity 100.0%; Pred. No. 4.5e-20;
Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	TGTACAGACCCAAACAACATACAAAGAAAAGTATCCCTATCCAGAGGACCGGAGA Db	1	TGTACAGACCCAAACAACATACAAAGAAAAGTATCCCTATCCAGAGGACCGGAGA 			
RESULT 4							
HIV3168		HIV3168 108 bp DNA linear VRL 02-AUG-1993		QY	1	TGTACAGACCCAAACAACATACAAAGAAAAGTATCCCTATCCAGAGGACCGGAGA 60 Db	1
LOCUS		Human immunodeficiency virus type 1 (HIV-1) envelope gene V3		Db	1	TGTACAGACCCAAACAACATACAAAGAAAAGTATCCCTATCCAGAGGACCGGAGA 60 	
DEFINITION		region, partial cds.		QY	61	GCATTGGTACATAATTAGGAAATAATGAGAACATTGT 108 Db	61
ACCESSION	M61584	M37886		Db	61	GCATTGGTACATAATTAGGAAATAATGAGAACATTGT 108 	
VERSION	M61584.1	GT:329219					
SOURCE		envelope-associated protein.					
ORGANISM		Human immunodeficiency virus 1 (HIV-1)					
		Human immunodeficiency virus 1					
		Viruses; Retroviridae; Lentivirus; Primate lentivirus group.					
REFERENCE	1.	(bases 1 to 108)					
AUTHORS	Larosa, G.J., Davide, J.P., Weinhold, K., Waterbury, J.A., Profy, A.T., Lewis, J.A., Langlois, A.J., Dreesman, G.R., Boswell, R.N., Shadduck, P., Holley, L.H., Karplus, M., Bolognesi, D.P., Matthews, T.J., Emini, E.A., and Putney, S.D.						
TITLE	Conserved sequence and structural elements in the HIV-1 principal neutralizing determinant						
JOURNAL	Science	263 (4524), 932-935 (1990)					
MEDLINE	90364416						
PUBMED	2392605						
2.	(sites)						
AUTHORS	Larosa, G.J., Davide, J.P., Weinhold, K., Waterbury, J.A., Profy, A.T., Lewis, J.A., Langlois, A.J., Dreesman, G.R., Boswell, R.N., Shadduck, P., Holley, L.H., Karplus, M., Bolognesi, D.P., Matthews, T.J., Emini, E.A., and Putney, S.D.						
TITLE	Conserved sequence and structural elements in the HIV-1 principal neutralizing determinant: corrections and clarifications						
JOURNAL	Science	251 (495), 811 (1991)					
MEDLINE	91118022						
PUBMED	1990444						
REFERENCE	3.	(sites)					
AUTHORS	Larosa, G.J., Weinhold, K., Profy, A.T., Langlois, A.J., Dreesman, G.R., Boswell, R.N., Shadduck, P., Bolognesi, D.P., Matthews, T.J., Emini, E.A., and Putney, S.D.						
TITLE	Conserved sequence and structural elements in the HIV-1 principal neutralizing determinant: further clarifications						
JOURNAL	Science	253 (5024), 1146 (1991)					
MEDLINE	91361090						
PUBMED	1887238						
COMMENT	Original source text: Human immunodeficiency virus type 1 V3 region proviral DNA.						
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gene	1..108		1..108				
CDS	1..108						
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			/gene="env"				
			/codon_start=1				
			/product="envelope protein"				
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			Query Match Score 108; DB 14; Length 108;				
			Best Local Similarity 100.0%; Pred. No. 4..5e-20;				
			Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				

RESULT 6		HIVV3170		108 bp DNA linear VRL 02-AUG-1993			
	DEFINITION	Human immunodeficiency virus type 1 (HIV-1) envelope Gene V3					
ACCESSION	M61586 M37586	region, partial cds.					
VERSION	M61586.1	GI:329223					
KEYWORDS		envelope-associated protein.					
ORGANISM		Human immunodeficiency virus 1 (HIV-1)					
REFERENCE		Viruses; Retroviridae; Lentivirus; Primate lentivirus group.					
AUTHORS	Larosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T., Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N., Shadduck,P., Holley,L.H., Karplus,M., Bolognesi,D.P., Matthews,T.J., Emini,E.A. and Putney,S.D.	1. (bases 1 to 108)					
TITLE	Conserved sequence and structural elements in the HIV-1 principal neutralizing determinant	2. (sites)					
JOURNAL	Science 249 (4971), 932-935 (1990)	2. (sites)					
MEDLINE	90364416	2392/85					
PUBMED	19904446						
REFERENCE							
AUTHORS	Larosa,G.J., Davide,J.P., Weinhold,K., Waterbury,J.A., Profy,A.T., Lewis,J.A., Langlois,A.J., Dreesman,G.R., Boswell,R.N., Shadduck,P., Holley,L.H., Karplus,M., Bolognesi,D.P., Matthews,T.J., Emini,E.A. and Putney,S.D.	3. (sites)					
TITLE	Conserved sequence and structural elements in the HIV-1 principal neutralizing determinant: corrections and clarifications	3. (sites)					
JOURNAL	Science 251 (4995), 811 (1991)	3. (sites)					
MEDLINE	91116022	19904446					
PUBMED	1887338						
COMMENT	Original source text: Human immunodeficiency virus type 1 V3 region proviral DNA, sibling of 153 and 185.						
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		Location/Qualifiers					
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ORIGIN							
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ORIGIN							
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CDS							
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		Best Local Similarity 100.0%; Pred. No. 4.5e-20;					
		Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					

HIVC3AA	HIVC3AA	126 bp ss-RNA linear	VRL 02-AUG-1993	Nature 313 (6002), 450-458 (1985)
LOCUS	Human immunodeficiency virus type 1 envelope gene v3 region, partial cds			JOURNAL MEDLINE 2982104 PUBMED 3 (bases 1 to 276)
DEFINITION				REFERENCE Wain-Hobson, S., Vartanian, J.-P., Henry, M., Chenciner, N., M64768 VERNER, M.-T., Sala, M., Nugeyre, M.-T., Cheynier, R., Delassus, S., Martins, L.P., Guetard, D., Klatzmann, D., Gluckman, J.-C., Rosenbaum, W., SOURCE Human immunodeficiency virus 1 (HIV-1) ORGANISM Human immunodeficiency virus 1 Viruses; Retrovirus; Retroviridae; Lentivirus; Primate lentivirus group.
ACCESSION	M64768	GI:326450		AUTHORS Barre-Sinoussi, F. and Montagnier, L. TITLE LAV revisited: origins of the early HIV-1 isolates from Institut Pasteur JOURNAL Science 252 (5008), 961-965 (1991)
KEYWORDS	envelope-associated protein.			2035026 JOURNAL MEDLINE 91240282 PUBMED 4 (bases 1 to 276)
SOURCE	Human immunodeficiency virus 1			REFERENCE Lukašov, V.V. and Goudsmit, J.
ORGANISM	Human immunodeficiency virus 1			TITLE Increasing genotypic and phenotypic selection from the original genomic RNA populations of HIV-1 strains LAI and MN (NM) by peripheral blood mononuclear cell culture, B-cell-line propagation and T-cell-line adaptation
ACCESSION	1 (bases 1 to 126)			JOURNAL AIDS 9 (12), 1307-1311 (1995)
REFERENCE	Nara, P.L., Smit, L., Dunlop, N., Hatch, W., Merges, M., Waters, D., Kelliber, J., Gallo, R.C., Fischliger, P.J. and Goudsmit, J.			2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
AUTHORS	Title			Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
KEYWORDS	Emergence of viruses resistant to neutralization by V3-specific antibodies in experimental human immunodeficiency virus type 1 IIIB infection of chimpanzees			LOCATION/QUALIFIERS (individual isolate Patient LAI) cDNA to genomic RNA.
JOURNAL	J. Virol. 64 (8), 3779-3791 (1990)			FEATURES source
MEDLINE	90117876			1. organism="Human immunodeficiency virus 1" /mol type="genomic RNA" /db xref="taxon:11676"
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Matches	108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			TITLE Increasing genotypic and phenotypic selection from the original genomic RNA populations of HIV-1 strains LAI and MN (NM) by peripheral blood mononuclear cell culture, B-cell-line propagation and T-cell-line adaptation
Db	19	TGTACAGACCACAACTAACATAAGAAAGTATCGTATCCAGAGGACCGGGAGA 60		JOURNAL AIDS 9 (12), 1307-1311 (1995)
Qy	1	TGTACAGACCACAACTAACATAAGAAAGTATCGTATCCAGAGGACCGGGAGA 60		2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
Db	19	TGTACAGACCACAACTAACATAAGAAAGTATCGTATCCAGAGGACCGGGAGA 78		Original Best Local Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	TGTACAGACCACAACTAACATAAGAAAGTATCGTATCCAGAGGACCGGGAGA 78		2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
Db	19	TGTACAGACCACAACTAACATAAGAAAGTATCGTATCCAGAGGACCGGGAGA 78		Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	61	GCATTCTTACATAGGAAATAATAGGAAATATGAGACAAGACATTTG 108		2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
Db	79	GCATTCTTACATAGGAAATAATAGGAAATATGAGACAAGACATTTG 126		Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1	TGTACAGACCACAACTAACATAAGAAAGTATCGTATCCAGAGGACCGGGAGA 126		2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
Db	79	TGTACAGACCACAACTAACATAAGAAAGTATCGTATCCAGAGGACCGGGAGA 138		Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT	9			2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
LOCUS	HIV1AIC21A	276 bp ss-RNA linear	VRL 11-APR-1996	Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DEFINITION	Human immunodeficiency virus type 1 (isolate LAic21) envelope glycoprotein gp120 (env) gene, V3 region.			2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
VERSION	L48399	GI:1048695		Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
KEYWORDS	envelope glycoprotein; variable domain III.			2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
ORGANISM	Human immunodeficiency virus 1			Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ACCESSION	L48399.1	GI:1048695		2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
REFERENCE	Wain-Hobson, S., Sonigo, P., Danos, O., Cole, S. and Alizon, M.			Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AUTHORS	Nucleotide sequence of the AIDS virus, LAV			2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
TITLE	Cell 40 (1), 9-17 (1985)			Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
JOURNAL				2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
MEDLINE	85039333			Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PUBMED	2981635			2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
REFERENCE	Muesing, M.A., Smith, D.H., Cabradilla, C.D., Benton, C.V., Lasky, L.A. and Capon, D.J.			Query Match Similarity 100.0%; Score 108; DB 14; Length 276; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
AUTHORS	Nucleic acid structure and expression of the human AIDS/lymphadenopathy retrovirus			2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.
TITLE				2035026 JOURNAL MEDLINE 96188304 PUBMED 8605049 COMMENT Original source text: Human immunodeficiency virus type 1 (strain IIIB/H9) viral RNA, clone C3.

Domingo, E. Point mutant frequencies in the pol gene of human immunodeficiency virus type 1 are two- to threefold lower than those of env AIDS Res. Hum. Retroviruses 12 (12), 1117-1128 (1996)

ORIGIN

source 1..288 /organism="unknown" /mol_type="unassigned DNA"

Query Match 100.0%; Score 108; DB 6; Length 288; Best Local Similarity 100.0%; Pred. No. 4.3e-20; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Quy 1 TGTACAAGCCAAACATAAGAAAAGATCCGATCCAGAGCAGGGAGA 60 Db 115 TGTACAAGCCAAACATAAGAAAAGATCCGATCCAGAGCAGGGAGA 174

Quy 61 GCATTGTACAACTAGGAAAAATAAGGAAATATGAGAACAGCATTT 108 Db 175 GCATTGTACAACTAGGAAAAATAAGGAAATATGAGAACAGCATTT 222

RESULT 11

LOCUS 105603 318 bp DNA linear PAT 02-DEC-1994 DEFINITION Sequence 9 from Patent EP 0306219.

ACCESSION 105603 VERSION 105603.1 GI:590567

KEYWORDS Unknown.

SOURCE Unclassified.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 318) Rusch, J.R., Punney, S.D., Javaherian, K., Farley, J., Grimalia, R., Lynn, D., Petro, J. and O'Keefe, T.

TITLE Novel HIV proteins and peptides useful in the diagnosis, prophylaxis or therapy of AIDS

JOURNAL Patent : EP 0306219-A2 9 08-MAR-1989; Location/Qualifiers 1..318

FEATURES source /organism="unknown" /mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 108; DB 6; Length 318; Best Local Similarity 100.0%; Pred. No. 4.3e-20; Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Quy 1 TGTACAAGCCAAACATAAGAAAAGATCCGATCCAGAGCAGGGAGA 60 Db 25 TGTACAAGCCAAACATAAGAAAAGATCCGATCCAGAGCAGGGAGA 84

Quy 61 GCATTGTACAACTAGGAAAAATAAGGAAATATGAGAACAGCATTT 108 Db 85 GCATTGTACAACTAGGAAAAATAAGGAAATATGAGAACAGCATTT 132

RESULT 12 HIV1U40538 405 bp DNA linear VRL 12-OCT-1996

LOCUS Human immunodeficiency virus type 1 isolate D22/+28 envelope DEFINITION Glycoprotein gp120 (env) gene, c2v3 region, partial cds.

ACCESSION U40538 VERSION U40538.1 GI:1620476

KEYWORDS Human immunodeficiency virus 1 (HIV-1)

ORGANISM Human immunodeficiency virus 1 (HIV-1) Lentiviridae; Lentivirus; Primate Viruses; Retroid viruses; Retroviridae; Lentivirus; Primate Lentivirus group.

REFERENCE 1 (bases 1 to 405) Quinones-Mateu, M.E., Holguin, A., Soriano, V. and Domingo, E.

TITLE env gene diversity of HIV type 1 isolates from Spain

JOURNAL AIDS Res. Hum. Retroviruses 12 (10), 955-957 (1996)

MEDLINE 96392169

PUBMED 8798981

REFERENCE 2 (bases 198 to 331) Quinones-Mateu, M.E., Holguin, A., Dopazo, J., Najera, I. and Domingo, E.

TITLE Point mutant frequencies in the pol gene of human immunodeficiency virus type 1 are two- to threefold lower than those of env AIDS Res. Hum. Retroviruses 12 (12), 1117-1128 (1996)

JOURNAL

MEDLINE 97000986
 PUBMED 8844016
 REFERENCE 3 (bases 1 to 405)
 AUTHORS Quinones-Mateu,M.E.
 TITLE Direct Submission
 JOURNAL Submitted (13-NOV-1995) Miguel E. Quinones-Mateu, Centro de Biologia Molecular 'Severo Ochoa', Universidad Autonoma de Madrid, Cantoblanco, Madrid, 28049, Spain
 COMMENT On Oct 16, 1996 this sequence version replaced gi:1304537.
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 /proviral
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 /isolate="D22,+48"
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 PNNNTRKSIRIQRGPGRFTVIGKGNMROHC"
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 Best Local Similarity 100.0%; Pred. No. 4_2e-20;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTACAGACCCAAACACATAACAGAAAAGTATCGTATCCAGAGGACCAGGGAGA 60
 Db 25 TGTACAGACCCAAACACATAACAGAAAAGTATCGTATCCAGAGGACCAGGGAGA 84
 QY 61 GCATTGTTACAATAGAAATATGAAATATGAAAGGACATGT 108
 Db 85 GCATTGTTACAATAGAAATATGAAATATGAAAGGACATGT 132
 Search completed: March 11, 2004, 21:24:04
 Job time : 680.083 secs

RESULT 14
 I05605 LOCUS I05605 423 bp DNA linear PAT 02-DEC-1994
 DEFINITION Sequence 11 from Patent EP 0306219.
 ACCESSION I05605
 VERSION I05605.1 GI:590568
 KEYWORDS Unknown.
 SOURCE Unkown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 423)
 AUTHORS Ruscica,J.R., Putney,S.D., Javaherian,K., Farley,J., Grimalis,R., Lynn,D., Petro,J., and O'reefee,T.
 TITLE Novel HIV Protease Inhibitor Composed of the Dipeptidyl Peptidase IV Inhibitor Dapivirozine and a Peptide Consisting of the Dipeptidyl Peptidase IV Inhibitor Dapivirozine and a Peptide Consisting of the Dipeptidyl Peptidase IV Inhibitor Dapivirozine
 FEATURES source
 source
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 /mol_type="unassigned DNA"
 ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 4_2e-20;
 Matches 108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGTACAGACCCAAACACATAACAGAAAAGTATCGTATCCAGAGGACCAGGGAGA 60

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 18:51:27 ; Search time 304.156 seconds
 Perfect score: 1801.765 Million cell updates/sec

Title: US-10-003-035-75
 Sequence: 1 ttattccataatgtatgtttagg.....acctcccaatcccgaggaa 129

Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 3378863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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- 2: Genesegn1980s:*
- 3: Genesegn2000s:*
- 4: Genesegn2001as:*
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- 6: Genesegn2002as:*
- 7: Genesegn2003as:*
- 8: Genesegn2003bs:*
- 9: Genesegn2003cs:*
- 10: Genesegn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	12.9	100.0	129	9 ADB87802	Adb87802 gp41 transmembrane domain DNA.
2	12.9	100.0	129	9 ADD66326	Add66326 HIV gp41
3	12.9	100.0	615	9 ADB87771	Adb87771 HIV-1 p17
4	12.9	100.0	615	9 ADD66293	Add66293 HIV p17 m
5	12.9	100.0	915	9 ADB87777	Adb87777 HIV-1 p24
6	12.9	100.0	915	9 ADD66299	Add66299 HIV p24 m
7	12.9	100.0	1026	2 AAQ03968	Aaq03968 panv9 enc
8	12.9	100.0	1026	2 AAC28095	Aac28095 Recombinant
9	12.9	100.0	1308	9 ADB87765	Adb87765 HIV-1 p17
10	12.9	100.0	1308	9 ADD66287	Add66287 HIV p17/2
11	12.9	100.0	2237	1 AAN90531	Aan90531 Sequence
12	12.9	100.0	2280	9 ADB87745	Adb87745 HIV-1 str
13	12.9	100.0	2280	9 ADD66267	Add66267 HIV clone
14	12.9	100.0	2553	1 AAN80949	Aan80949 HIV protein
15	12.9	100.0	2583	9 ADB87753	Adb87753 HIV-1 BH1
16	12.9	100.0	2583	9 ADD66275	Add66275 HIV B_m/B
17	12.9	100.0	2747	9 ADB87752	Adb87752 HIV-1 BH1
18	12.9	100.0	2747	9 ADD66274	Add66274 HIV E_mde
19	12.9	100.0	2945	2 AAT05127	Aat05127 HIV virus
20	12.9	100.0	2950	9 ADB87751	Adb87751 HIV-1 BH1
21	12.9	100.0	2950	9 ADD66273	Add66273 HIV E_mde
22	12.9	100.0	3156	1 AAN60128	Aan60128 Sequence
23	12.9	100.0	3157	9 ADB87743	Adb87743 HIV-1 str

RESULT 1
 ID ADB87802 standard; DNA; 129 BP.

XX AC ADB87802;

XX DT 04-DEC-2003 (first entry)

DE DE gp41 transmembrane domain DNA.

XX KW adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoa; cytotoxic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.

KW KW Human immunodeficiency virus 1.

XX OS Human immunodeficiency virus 1.

XX PN US2002155127-A1.

XX PD 24-OCT-2002.

XX XX

PF PF 01-NOV-2001; 2001US-00003035.

XX PR PR 02-JUN-2000; 2000US-00585599.

XX PR 04-JUN-2001; 2001WO-US018238.

XX (WANG/) WANG D.

XX PI Wang D.

XX DR WPI; 2003-182621/18.

XX PT New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of pathogenic

PT antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor

PT antigens.

XX PS Claim 24; Page 81; 156pp; English.

XX CC This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoa, cytotoxic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against

infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the invention.

XX Sequence 129 BP; 34 A; 22 C; 31 G; 42 T; 0 U; 0 Other;
 Query Match 100.0%; Score 129; DB 9; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.1e-30;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC

Qy 1 TTATCCATAATGATAGTGGCTTTAGAGAATAGTTTGCTGTACTTCT 60
 Db 1 TTATCCATAATGATAGTGGCTTTAGAGAATAGTTTGCTGTACTTCT 60
 Qy 61 GTAGGAAATAGTAGTGGCAGGATTACCATTAATCGTTTCAGMCCACCTCCAAATC 120
 Db 1 GTAGGAAATAGTAGTGGCAGGATTACCATTAATCGTTTCAGMCCACCTCCAAATC 120
 Qy 61 GTAGTGAATAAGTAGTGGCAGGATTACCATTAATCGTTTCAGACCCACCTCCAAATC 120
 Db 61 GTAGTGAATAAGTAGTGGCAGGATTACCATTAATCGTTTCAGACCCACCTCCAAATC 120
 Qy 121 CGAGGGGA 129
 Db 121 CGAGGGGA 129

RESULT 3

ADBB87771 standard; DNA; 615 BP.
 XX ID ADBB87771;
 AC ADBB87771;
 XX DT 04-DEC-2003 (first entry)
 XX DE HIV-1 p17 membrane form DNA SEQ ID 42.
 XX ADDB66326 standard; DNA; 129 BP.
 XX AC ADDB66326;
 XX DT 15-JAN-2004 (first entry)
 XX DE gp41 transmembrane domain DNA.
 XX KW hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
 XX KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
 XX KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
 XX HIV infection; ds.
 OS Human immunodeficiency virus 1.
 XX PN US2002155127-A1.
 XX PD 24-OCT-2002.
 XX PF 01-NOV-2001; 2001US-00003035.
 XX PR 02-JUN-2000; 2000US-0058599.
 XX PR 04-JUN-2001; 2001WO-US018238.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-182621/18.
 XX PP 17-MAR-2003; 2003US-00286332.
 XX PR 02-JUN-2000; 2000US-0058599.
 XX PR 04-JUN-2001; 2001WO-US018238.
 XX PR 01-NOV-2001; 2001US-00003035.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-851718/79.

XX Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant adenovirus.

XX Example: SEQ ID NO 75; 185pp; English.
 PS The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence

CC is used in the exemplification of the invention.

XX Sequence 129 BP; 34 A; 22 C; 31 G; 42 T; 0 U; 0 Other;
 Query Match 100.0%; Score 129; DB 9; Length 129;
 Best Local Similarity 100.0%; Pred. No. 1.1e-30;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC

Qy 1 TTATCCATAATGATAGTGGCTTTAGAGAATAGTTTGCTGTACTTCT 60
 Db 1 TTATCCATAATGATAGTGGCTTTAGAGAATAGTTTGCTGTACTTCT 60
 Qy 61 GTAGGAAATAGTAGTGGCAGGATTACCATTAATCGTTTCAGMCCACCTCCAAATC 120
 Db 61 GTAGGAAATAGTAGTGGCAGGATTACCATTAATCGTTTCAGMCCACCTCCAAATC 120
 Qy 121 CGAGGGGA 129
 Db 121 CGAGGGGA 129

RESULT 3

ADBB87771 standard; DNA; 615 BP.
 XX ID ADBB87771;
 AC ADBB87771;
 XX DT 04-DEC-2003 (first entry)
 XX DE HIV-1 p17 membrane form DNA SEQ ID 42.
 XX XX HIV-1 p17 membrane form DNA SEQ ID 42.
 XX DE HIV-1 p17 membrane form DNA SEQ ID 42.
 XX KW adenovirus; HIV antigen; infection; anti HIV; virucide; antibacterial;
 XX KW antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
 XX KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
 OS Human immunodeficiency virus 1.
 XX PN US2002155127-A1.
 XX PD 24-OCT-2002.
 XX PF 01-NOV-2001; 2001US-00003035.
 XX PR 02-JUN-2000; 2000US-0058599.
 XX PR 04-JUN-2001; 2001WO-US018238.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-182621/18.
 XX PP 17-MAR-2003; 2003US-00286332.
 XX PR 02-JUN-2000; 2000US-0058599.
 XX PR 04-JUN-2001; 2001WO-US018238.
 XX PR 01-NOV-2001; 2001US-00003035.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-851718/79.

CC This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding an HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen in a host upon infection of the host by the recombinant adenovirus. The products of the invention have anti-HIV, virucide, antibacterial, antiparasitic, protozoacide, cytostatic and immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic virus, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumour antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the

CC invention.
 XX Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 129; DB 9; Length 615;
 Best Local Similarity 100.0%; Pred. No. 1.6e-30;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTCAATGATACTAGCAGGCTTGGAGTTAACATACTTTTGCTGACTTCT 60
 DB 484 TTATTCAATGATACTAGCAGGCTTGGAGTTAACATACTTTTGCTGACTTCT 543
 QY 61 GTAGTGAATAGACTAGCTTACCGGATTCACATTATGGTTCAAGACCCACCTCCAAATC 120
 DB 544 GTAGTGAATAGACTAGCTTACCGGATTCACATTATGGTTCAAGACCCACCTCCAAATC 603
 QY 121 CGAGGGAA 129
 DB 604 CGAGGGAA 612

RESULT 5
 ADD6293 standard; DNA; 915 BP.
 ID ADB87777 standard; DNA; 915 BP.
 XX ADB87777;
 AC ADB87777;
 DT 04-DEC-2003 (first entry)
 DE HIV-1 D24 membrane form DNA SEQ ID 48.
 XX HIV antigen; infection; anti-HIV; virucide; antibacterial;
 KW antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
 KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
 XX Human immunodeficiency virus 1.
 OS US2002155127-A1.
 PN XX
 PD 24-OCT-2002.
 DE XX
 PR 01-NOV-2001; 2001US-00003035.
 DE HIV p17 membrane form DNA.
 XX PR 02-JUN-2000; 2000US-00585599.
 DE HIV; hepatitis; Marburg; Arbovirus; hepatitis;
 KW respiratory syncytial virus; human papilloma virus;
 KW infection; ds; gene.
 XX PR 04-JUN-2001; 2001WO-US018238.
 DE Human immunodeficiency virus.
 OS XX
 PN (WANG/) WANG D.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-182621/18.
 XX PT New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against HIV antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor antigens.
 XX PT PR 02-JUN-2000; 2000US-00286332.
 XX PT PR 04-JUN-2001; 2001WO-US018238.
 XX PT PR 01-NOV-2001; 2001US-00003035.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-851718/79.
 DR P-PSDB; ADD6293;
 XX Enhancing the immunity of a host to infection of a first and second or pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant adenovirus.
 XX PS Example; SEQ ID NO 42; 185pp; English.
 XX The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
 XX SQ Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
 Query Match 100.0%; Score 129; DB 9; Length 615;
 SQ Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
 Query Match 100.0%; Score 129; DB 9; Length 915;

Best Local Similarity 100.0%; Pred. No. 1.6e-30;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TTATTCAATGATACTAGCAGGCTTGGAGTTAACATACTTTTGCTGACTTCT 60
 DB 484 TTATTCAATGATACTAGCAGGCTTGGAGTTAACATACTTTTGCTGACTTCT 543
 QY 61 GTAGTGAATAGACTAGCTTACCGGATTCACATTATGGTTCAAGACCCACCTCCAAATC 120
 DB 544 GTAGTGAATAGACTAGCTTACCGGATTCACATTATGGTTCAAGACCCACCTCCAAATC 603
 QY 121 CGAGGGAA 129
 DB 604 CGAGGGAA 612

RESULT 5
 ADD6293 standard; DNA; 915 BP.
 ID ADB87777 (first entry)
 XX ADB87777;
 AC ADB87777;
 DT 04-DEC-2003 (first entry)
 DE HIV-1 D24 membrane form DNA SEQ ID 48.
 XX HIV antigen; infection; anti-HIV; virucide; antibacterial;
 KW antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
 KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
 XX Human immunodeficiency virus 1.
 OS US2002155127-A1.
 PN XX
 PD 24-OCT-2002.
 DE XX
 PR 01-NOV-2001; 2001US-00003035.
 DE HIV p17 membrane form DNA.
 XX PR 02-JUN-2000; 2000US-00585599.
 DE HIV; hepatitis; Marburg; Arbovirus; hepatitis;
 KW respiratory syncytial virus; human papilloma virus;
 KW infection; ds; gene.
 XX PR 04-JUN-2001; 2001WO-US018238.
 DE Human immunodeficiency virus.
 OS XX
 PN (WANG/) WANG D.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-182621/18.
 XX PT New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against HIV antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E, or tumor antigens.
 XX PT PR 02-JUN-2000; 2000US-00286332.
 XX PT PR 04-JUN-2001; 2001WO-US018238.
 XX PT PR 01-NOV-2001; 2001US-00003035.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-851718/79.
 DR P-PSDB; ADD6293;
 XX Enhancing the immunity of a host to infection of a first and second or pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprises administering to the host a first and a second recombinant adenovirus.
 XX PS Example; SEQ ID NO 42; 185pp; English.
 XX The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
 XX SQ Sequence 615 BP; 217 A; 101 C; 162 G; 135 T; 0 U; 0 Other;
 Query Match 100.0%; Score 129; DB 9; Length 615;
 SQ Sequence 915 BP; 314 A; 168 C; 229 G; 204 T; 0 U; 0 Other;
 Query Match 100.0%; Score 129; DB 9; Length 915;

Best Local Similarity 100.0%; Pred. No. 1.8e-30; Mismatches 0; Indels 0; Gaps 0;

Matches 129; Conservative 0; No. 1.8e-30; Mismatches 0; Indels 0; Gaps 0;

Db 784 TTATTCAATAATGATAAGTAGGGCTTGGTAGGTTAAAGAATAAGTTTGCTGTACTTCTC 843

Qy 1 TTATTCATTAATGATAAGTAGGGCTTGGTAGGTTAAAGAATAAGTTTGCTGTACTTCTC 60

Db 784 TTATTCATTAATGATAAGTAGGGCTTGGTAGGTTAAAGAATAAGTTTGCTGTACTTCTC 120

Db 784 TTATTCATTAATGATAAGTAGGGCTTGGTAGGTTAAAGAATAAGTTTGCTGTACTTCTC 843

Qy 61 GTAGTGAATAGACTTGGCAGGGATAATTCCACATTAGTGTGTTAGAACCCACCTCCAACTC 120

Db 844 GTAGTGAATAGACTTGGCAGGGATAATTCCACATTAGTGTGTTAGAACCCACCTCCAACTC 903

Qy 121 CGGAGGGAA 129

Db 904 CGGAGGGAA 912

RESULT 7

ID AAQ03968 standard; DNA; 1026 BP.

XX AAQ03968;

XX DT 04-SEP-1990 (first entry)

XX DE pENV9 encoding a recombinant peptide with HIV antigenicity.

XX KW human immunodeficiency virus; antigenicity; gp120; gp41; poliovirus.

XX DE HIV p24 membrane form DNA.

XX OS Synthetic.

XX PN US4861707-A.

XX PD 29-AUG-1989.

XX PF 02-FEB-1987; 87US-00010056.

XX PR 02-FEB-1987; 87US-00010056.

XX PA (DUPO) DU PONT DE NEMOURS & CO E I.

XX PI Ivanoff LA, Petteway SR;

XX DR WPI; 1990-122902/16.

XX PR P-PSDB; AA04019.

XX PT Recombinant peptide with antigenicity of human immuno-deficiency virus - comprises forty-six amino acids from gp. 120 C-terminal and two hundred and forty amino acids from gp. 41 N-terminal.

XX PS Claim 1; Fig 4; 13pp; English.

XX CC The sequence encodes ENV9, a recombinant peptide. ENV9 consists of about 54 amino acids from the N-terminal of a poliovirus sequence (PEXC), as well as those regions of HIV gp120 and gp41 detailed above. ENV9 can be used to detect HIV antibodies. "False positive" results are minimised as it contains few non-critical antigens. It can also be used in a vaccine against HIV

XX SQ Sequence 1026 BP; 335 A; 178 C; 275 G; 238 T; 0 U; 0 Other;

XX Query Match Score 129; DB 2; Length 1026;

CC Best Local Similarity 100.0%; Pred. No. 1.8e-30;

CC Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTCAATAATGATAAGTAGGGCTTGGTAGGTTAAAGAATAAGTTTGCTGTACTTCTC 60

Db 820 TTATTCAATAATGATAAGTAGGGCTTGGTAGGTTAAAGAATAAGTTTGCTGTACTTCTC 879

Qy 61 GTAGTGAATAGACTTGGCAGGGATAATTCCACATTAGTGTGTTAGAACCCACCTCCAACTC 120

Db 880 GTAGTGAATAGACTTGGCAGGGATAATTCCACATTAGTGTGTTAGAACCCACCTCCAACTC 939

Qy 121 CGGAGGGAA 129

Db 940 CGGAGGGAA 948

Query Match Score 129; DB 9; Length 915;

CC Best Local Similarity 100.0%; Pred. No. 1.8e-30;

CC Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TTATTCAATAATGATAAGTAGGGCTTGGTAGGTTAAAGAATAAGTTTGCTGTACTTCTC 60

AAQ28095
ID AAQ28095 standard; DNA; 1026 BP.
XX
AC AAQ28095;
XX DT 25-MAR-2003 (revised)
DT 12-FEB-1993 (first entry)
XX Recombinant DNA encoding ENV9.
DE Poliovirus; HIV; human immunodeficiency virus; AIDS; gp120; gp41; ss.
XX OS Synthetic.
XX PN US5141861-A.
XX PD 25-AUG-1992.
XX PF 04-MAY-1989; 89US-00347004.
XX PR 02-FEB-1987; 87US-00010056.
XX PA (DUFO) DU PONT DE NEMOURS & CO E I.
XX PI Ivanoff LA, Petteway SR;
XX DR WPI; 1992-307861/37.
DR P-PSDB; AAR26787.
XX Nucleotide sequence encoding a HIV antigen - comprising the C-terminal region of Gp120 and N-terminal of Gp41. for use in diagnosis and in vaccines.
XX
Claim 3: Fig 4; 12PP; English.
CC The Plasmid pENV9 was constructed by ligating the BgIII/BamHI fragment (nt 7196-8053) of HIV clone lambda Bl10 with the BgIII/ BamHI vector fragment of pEXC. The prod. was used to transform E. coli strain HB101 and MM294. The transforms produced a protein ENV9 contg. 349 amino acids correpond. to 54 amino acids from the N-terminal of the gp120 domain of pEXC, 46 amino acids of the C-terminal of the gp120 domain and 240 amino acids of the N-terminal of the gp41 domain. The peptide comprises the early detection antigen from gp120 and a highly reactive antigen from gp41 thus providing broad sensitivity to HIV infection. The sensitivity of the peptides permits the detection of HIV infection using small amounts of diagnostic reagents. The peptides have improved stability as compared to larger antigenic segments and contain fewer noncritical antigens which minimises the possibility of false positive results in detection of HIV infection. The peptides can also be used in vaccines protective against HIV. (Updated on 25-MAR-2003 to correct PF field.)
XX
Sequence 1026 BP; 335 A; 178 C; 275 G; 238 T; 0 U; 0 Other;
Query Match 100.0%; Score 129; DB 2; Length 1026;
Best Local Similarity 100.0%; Pred. No. 1..8e-30;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTCATAATGATAGTAGTGGAGGTGGAGGTTAAGATAATGTTGCTGTACTTCT 60
Db 820 TTATTCATAATGATAGTAGTGGAGGTGGAGGTTAAGATAATGTTGCTGTACTTCT 879
QY 61 GTAGTGAAATAGAGTTAGGGAGGGATATTCACTATTATGTTCAAGACCACTTCCCACATC 120
Db 880 GTAGTGAAATAGAGTTAGGGAGGGATATTCACTATTATGTTCAAGACCCACCTTCCCACATC 939
QY 121 CCGAGGGGA 129
Db 940 CCGAGGGGA 948
XX
AC ADBB7765;
XX DT 04-DEC-2003 (first entry)
XX DE HIV-1 p17/24 membrane form DNA SEQ ID 36.
XX KW adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial; antiparasitic; protozoide; cytostatic; immunomodulatory; vaccine; pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
XX OS Human immunodeficiency virus 1.
XX PN US2002155127-A1.
XX PD 24-OCT-2002.
XX PF 01-NOV-2001; 2001US-00003035.
XX PR 02-JUN-2000; 2000US-00585599.
XX PR 04-JUN-2001; 2001WO-05018238.
XX PA (WANG/) WANG D.
XX PI Wang D;
XX DR WPI; 2003-182621/18.
XX New recombinant adenoviruses, useful as vaccines for eliciting immune response or conferring protection against infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C or E, or tumor antigens.
XX
Claim 30; Fig 50A; 15pp; English.
CC This invention describes a novel recombinant adenovirus comprising an HIV sequence encoding HIV antigen, where expression of the HIV antigen by the recombinant adenovirus elicits an immune response directed against the HIV antigen. The product of the invention have anti-HIV, virucide, antibacterial, antiparasitic, cytostatic, immunomodulatory activity. The recombinant adenoviruses are useful as vaccines for eliciting immune responses or conferring protection against a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B, C, D or E or tumor antigens. The recombinant adenoviruses are also useful as genetic vaccines against pathogenic bacteria, parasites or protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing the immunogenicity of the HIV antigens. This sequence represents an HIV-1 strain BH10 antigen construct described in the disclosure of the invention.
XX
Sequence 1308 BP; 473 A; 236 C; 326 G; 273 T; 0 U; 0 Other;
Query Match 100.0%; Score 129; DB 9; Length 1308;
Best Local Similarity 100.0%; Pred. No. 1..9e-30;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TTATTCATAATGATAGTAGTGGAGGTGGAGGTTAAGATAATGTTGCTGTACTTCT 60
Db 1177 TTATTCATAATGATAGTAGTGGAGGTGGAGGTTAAGATAATGTTGCTGTACTTCT 1236
QY 61 GAGTGATAGAGTTAGGGAGGGATATTCACTATTATGTTCAAGACCACTTCCCACATC 120
Db 1237 GAGTGATAGAGTTAGGGAGGGATATTCACTATTATGTTCAAGACCCACCTTCCCACATC 1296
QY 121 CCGAGGGGA 129
Db 1297 CCGAGGGGA 1305

RESULT 10
ADD66287
ID ADD66287 standard; DNA; 1308 BP.

RESULT 9
ADB87765
ID ADB87765 standard; DNA; 1308 BP.

XX 01-NOV-2001; 2001US-00003035.
 XX PD 24-JUL-2003.
 PF 17-MAR-2003; 2003US-00286332.
 PR 02-JUN-2000; 2000US-00585599.
 PR 02-JUN-2000; 2000US-00585599.
 PR 04-JUN-2001; 2001US-0018238.
 PR 01-NOV-2001; 2001US-00003035.
 XX PA (WANG/) WANG D.
 PI PA (WANG/) WANG D.
 XX DR Wang D;
 PI XX
 PT WPI; 2003-85171B/79.
 PT Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprising administering to the host a first and a second recombinant adenovirus.
 XX PS Example; SEQ ID NO 16; 185pp; English.
 CC The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
 CC Sequence 2280 BP; 802 A; 386 C; 534 G; 558 T; 0 U; 0 Other;
 CC Query Match 100.0%; Score 129; DB 9; Length 2280;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-30; Indels 0; Gaps 0;
 CC Matches 129; Conservative 0; Mismatches 0;
 CC Db 2056 TTATTCAATGATAAGGGCTGTAGTTAGAATAGTTTGCTGTACTTCT 60
 CC Qy 1 TTTATTCATATGATAAGGGCTGTAGTTAGAATAGTTTGCTGTACTTCT 60
 CC Db 2056 TTATTCAATGATAAGGGCTGTAGTTAGAATAGTTTGCTGTACTTCT 2115
 CC Qy 61 GTACTGAATAGAGTTAGGAGGATATTACATTATGTTAGACCCACCTCCAAATC 120
 CC Db 2116 GTACTGAATAGAGTTAGGAGGATATTACATTATGTTAGACCCACCTCCAAATC 2175
 CC Qy 121 CCGAGGGAA 129
 CC Db 2176 CCGAGGGAA 2184
 XX RESULT 14
 ID AAN80949 standard; DNA; 2553 BP.
 XX AC AAN80949;
 XX DT 24-OCT-2003 (revised)
 XX DT 25-MAR-2003 (revised)
 XX DT 15-NOV-1990 (first entry)
 XX DE HIV protein HT6.
 XX KW HIV; HT6; gp160; envelope protein; RF; AIDS; 96.
 XX OS Human immunodeficiency virus; variant RF.
 XX EP272858-A.
 XX 29-JUN-1988.
 XX PR 14-DEC-1987; 87EP-00310967.
 XX PR 15-DEC-1986; 86US-00941111.
 XX PR 31-AUG-1987; 87US-00094481.
 XX US2003138459-A1.

XX 01-NOV-2001; 2001US-00003035.
 XX PD 24-JUL-2003.
 PF 17-MAR-2003; 2003US-00286332.
 PR 02-JUN-2000; 2000US-00585599.
 PR 02-JUN-2000; 2000US-00585599.
 PR 04-JUN-2001; 2001US-0018238.
 PR 01-NOV-2001; 2001US-00003035.
 XX PA (WANG/) WANG D.
 XX DR Wang D;
 PI XX
 PT WPI; 2003-85171B/79.
 PT Enhancing the immunity of a host to infection of a first and second pathogenic virus, e.g. influenza, hepatitis, respiratory syncytial, or HIV infections comprising administering to the host a first and a second recombinant adenovirus.
 XX PS Example; SEQ ID NO 16; 185pp; English.
 CC The invention relates to a method of enhancing the immunity of a host to infection of a first and second pathogenic virus comprising administering to the host a first and a second recombinant adenovirus. The method is useful for enhancing immunity of the host to infections, e.g. influenza, Ebola, Marburg, Arbovirus, hepatitis, respiratory syncytial, herpes simplex or human papilloma virus or HIV infections. The present sequence is used in the exemplification of the invention.
 CC Sequence 2280 BP; 802 A; 386 C; 534 G; 558 T; 0 U; 0 Other;
 CC Query Match 100.0%; Score 129; DB 9; Length 2280;
 CC Best Local Similarity 100.0%; Pred. No. 2.2e-30; Indels 0; Gaps 0;
 CC Matches 129; Conservative 0; Mismatches 0;
 CC Db 2056 TTATTCAATGATAAGGGCTGTAGTTAGAATAGTTTGCTGTACTTCT 60
 CC Qy 1 TTTATTCATATGATAAGGGCTGTAGTTAGAATAGTTTGCTGTACTTCT 60
 CC Db 2056 TTATTCAATGATAAGGGCTGTAGTTAGAATAGTTTGCTGTACTTCT 2115
 CC Qy 61 GTACTGAATAGAGTTAGGAGGATATTACATTATGTTAGACCCACCTCCAAATC 120
 CC Db 2116 GTACTGAATAGAGTTAGGAGGATATTACATTATGTTAGACCCACCTCCAAATC 2175
 CC Qy 121 CCGAGGGAA 129
 CC Db 2176 CCGAGGGAA 2184
 XX RESULT 13
 ID ADD6267 standard; DNA; 2280 BP.
 XX AC ADD6267;
 XX DT 15-JAN-2004 (first entry)
 XX DE HIV clone BH10 Env_mdeltaCdeltaT_300 DNA.
 XX KW virucide; hepatotropic; RNA editing; GP gene; vaccine; immunity enhanced;
 KW infection; influenza; Ebola; Marburg; Arbovirus; hepatitis;
 KW respiratory syncytial virus; herpes simplex virus; human papilloma virus;
 KW HIV infection; ds;
 XX OS Human immunodeficiency virus.
 XX PR 14-DEC-1987; 87EP-00310967.
 XX PR 15-DEC-1986; 86US-00941111.
 XX PR 31-AUG-1987; 87US-00094481.
 XX US2003138459-A1.

PA (REPK) REPLIGEN CORP.
 XX
 PT Rusche J., Lynn D., Carson H., Putney S., Jellis CL;
 XX
 DR WPI; 1988-176944/26.
 DR P-PSDB, AA880967.
 XX
 PT Prodn. of recombinant HIV envelope proteins in insect cells - useful as
 PT vaccine against AIDS and for diagnosis and therapy.
 XX
 Disclosure; Page ?; 4pp; English.
 XX
 CC The sequence is the result of cloning a hybrid envelope gene from HIV
 variants BH10 and RF. A central portion of the RF gene was used, the rest
 being from a distantly related variant BH10. The resulting clone, pACH76
 produces a hybrid gp 160 envelope protein with novel immunological and
 CC antigenic characteristics. It may be used to as a vaccine and for
 CC diagnosis and therapy of AIDS. See also AAN80948. (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 24-OCT-2003 to standardise OS field)
 XX
 Sequence 2553 BP; 887 A; 430 C; 613 G; 623 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 129; DB 1; Length 2553;
 Best Local Similarity 100.0%; Pred. No. 2.2e-30;
 Matches 129; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 TTATTCAATGATAAGTAGGGCTTCTGGTAGTTAAGAAATAGTTTGTGACTTTCT 60
 Db 2035 TTATTCAATGATAAGTAGGGCTTCTGGTAGTTAAGAAATAGTTTGTGACTTTCT 2094
 Qy 61 GTAGTGAATAGAGTTAGGGAGGATAATTACCATTAATGTTCAAGCCACCTCCAAATC 120
 Db 2095 GTAGTGAATAGAGTTAGGGAGGATAATTACCATTAATGTTCAAGCCACCTCCAAATC 2154
 Qy 121 CGGAGGGGA 129
 Db 2155 CGGAGGGGA 2163

RESULT 15
 ADBB87753
 ID ADBB87753 standard; DNA; 2583 BP.
 AC ADBB87753;
 .XX DT 04-DEC-2003 (first entry)
 XX DE HIV-1 BH10 construct EM/Em SEQ ID 24.
 XX KW adenovirus; HIV antigen; infection; anti-HIV; virucide; antibacterial;
 KW antiparasitic; protozoacide; cytostatic; immunomodulatory; vaccine;
 KW pathogen; Ebola virus; hepatitis virus; tumour antigen; ds.
 XX OS Human immunodeficiency virus 1.
 PN US2002155127-A1.
 XX PD 24-OCT-2002.
 XX PF 01-NOV-2001; 2001US-00003035.
 XX PR 02-JUN-2000; 2000US-00585599.
 PR 04-JUN-2001; 2001WO-US018238.
 XX PA (WANG/) WANG D.
 XX PI Wang D;
 XX DR WPI; 2003-182621/18.
 XX PT New recombinant adenoviruses, useful as vaccines for eliciting immune
 PT response or conferring protection against infection of a pathogenic
 PT antigen, e.g. HIV, Ebola virus, hepatitis A, B, C or E, or tumor

PT antigens.
 XX
 PS Claim 12; Fig 47; 156pp; English.
 XX
 CC This invention describes a novel recombinant adenovirus comprising an HIV
 sequence encoding an HIV antigen, where expression of the HIV antigen by
 the recombinant adenovirus elicits an immune response directed against
 the HIV antigen in a host upon infection of the host by the recombinant
 adenovirus. The products of the invention have anti-HIV, virucide,
 CC antibacterial, antiparasitic, protozoacide, cytostatic and
 CC immunomodulatory activity. The recombinant adenoviruses are useful as
 CC vaccines for eliciting immune response or conferring protection against
 CC infection of a pathogenic antigen, e.g. HIV, Ebola virus, hepatitis A, B,
 CC C, D or E or tumour antigens. The recombinant adenoviruses are also
 CC useful as genetic vaccines against pathogenic bacteria, parasites or
 CC protozoans, e.g. malaria. The immuno-stimulators are useful for enhancing
 CC the immunogenicity of the HIV antigens. This sequence represents an HIV-1
 CC strain BH10 antigen construct described in the disclosure of the
 CC invention.

XX
 Sequence 2583 BP; 892 A; 441 C; 621 G; 629 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 129; DB 9; Length 2583;
 Best Local Similarity 100.0%; Pred. No. 2.2e-30;
 Matches 129; Conservative 0; Mismatches 0; Gaps 0;
 Qy 1 TTATTCAATGATAAGTAGGGCTTCTGGTAGTTAAGAAATAGTTTGTGACTTTCT 60
 Db 2062 TTATTCAATGATAAGTAGGGCTTCTGGTAGTTAAGAAATAGTTTGTGACTTTCT 2121
 Qy 61 GTAGTGAATAGAGTTAGGGAGGATAATTACCATTAATGTTCAAGCCACCTCCAAATC 120
 Db 2122 GTAGTGAATAGAGTTAGGGAGGATAATTACCATTAATGTTCAAGCCACCTCCAAATC 2181
 Qy 121 CGGAGGGGA 129
 Db 2182 CGGAGGGGA 2190

Search completed: March 11, 2004, 20:49:42
 Job time : 306.156 secs

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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 20:30:23 ; Search time 45.4128 Seconds
(without alignments)

Title: US-10-003-035-74

Perfect score: 90

Sequence: 1 atgaaatgttggatggaaaata.....tgttgatgtatctgttgtgtct 90

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database : Issued Patents NA:

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- 4: /cgcn2_6/.ptodata/2/ina/6B_COMB.seq:*
- 5: /cgcn2_6/.ptodata/2/ina/PCTUS_COMB.seq:*
- 6: /cgcn2_6/.ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description	
1	90	100.0	105	1	US-08-029-402-14	Sequence 14, App1	
2	90	100.0	2020	2	US-08-417-2104-135	Sequence 135, App1	
3	90	100.0	2020	4	US-09-136-159A-135	Sequence 135, App1	
4	90	100.0	2028	2	US-08-417-2104-138	Sequence 138, App1	
5	90	100.0	2028	4	US-09-136-159A-138	Sequence 138, App1	
6	90	100.0	2050	2	US-08-417-2104-141	Sequence 141, App1	
7	90	100.0	2050	4	US-09-136-159A-141	Sequence 141, App1	
8	90	100.0	2571	2	US-07-916-098A-1	Sequence 1, App1	
9	90	100.0	2694	1	US-08-147-890-1	Sequence 1, App1	
10	90	100.0	2696	4	US-09-136-159A-1	Sequence 1, App1	
11	90	100.0	2730	3	US-08-728-122-1	Sequence 1, App1	
12	90	100.0	2945	6	5467872-1	Patent No. 5462872	
13	90	100.0	3084	1	US-08-147-890-2	Sequence 2, App1	
14	90	100.0	3084	3	US-08-463-210-6	Sequence 6, App1	
15	90	100.0	3563	4	US-08-463-028-6	Sequence 6, App1	
C	17	90	100.0	3807	2	US-08-41-2104-78	Sequence 78, App1
C	17	90	100.0	3807	4	US-09-136-159A-78	Sequence 1, App1
22	90	100.0	8913	3	US-09-124-900-1	Sequence 1, App1	
23	90	100.0	8913	4	US-08-620-958A-9	Sequence 9, App1	
24	90	100.0	8913	3	US-09-620-958A-4	Sequence 4, App1	
25	88.4	98.2	8913	3	US-09-620-958A-3	Sequence 3, App1	
26	86.8	96.4	2531	3	US-07-955-483-18	Sequence 4, App1	
27	86.8	96.4	2644	3	US-08-472-240A-9	Sequence 9, App1	

ALIGNMENTS

RESULT 01
US-08-029-402-14
; Sequence 14 Application US-08029-02
; Patent No. 5462872
; GENERAL INFORMATION:
; APPLICANT: Murphy, Cherry I.
; TITLE OF INVENTION: Baculovirus Vectors For Expression of Secretory and Membrane-Bound Proteins
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox
; STREET: 1225 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Parent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/029,402
; FILING DATE: 1993/03/05
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: FOX, Samuel L.
; REGISTRATION NUMBER: 30,353
; REFERENCE/DOCKET NUMBER: 0614.0860001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 466-0800
; TELEX/FAX: (202) 813-8716
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 105 base pairs
; TYPE: NUCLEAR ACID
; STRANDEDNESS: both
; TOPOLOGY: linear
; FEATURES:
; NAME/KEY: CDS
; LOCATION: 10..105
; US-08-029-402-14
Query Match 100.0%; Score 90; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 2-2a-1;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGTGAAGGAGAAATTCAGACTTGAGATGGGTGAGATGGCAACATG 60

Db 10 ATGAGAGTGAAGGAAATAATCAGGACTTGTGGAGATGGGGTGGAGATGGGGACCATG 69
 Qy 61 CTCCTGGATGTGATGATCTGTAGTGTCT 90
 Db 70 CTCCCTGGATGTGATGATCTGTAGTGTCT 99

RESULT 2
 US 09-417-210A-135
 i Sequence 135, Application US/08417210A
 i Patent No. 5863542
 i GENERAL INFORMATION:
 i APPLICANT: PAOLETTI, ENZO
 i APPLICANT: TARTAGLIA, JAMES S
 i APPLICANT: COX, WILLIAM I.
 i TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
 i NUMBER OF SEQUENCES: 148
 i CORRESPONDENCE ADDRESS:
 i ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
 i STREET: 530 FIFTH AVENUE
 i CITY: NEW YORK
 i STATE: NEW YORK
 i COUNTRY: USA
 i ZIP: 10036
 COMPUTER READABLE FORM:
 i MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentn Release #1.0, Version #1.3.0
 CURRENT APPLICATION DATA:
 i APPLICATION NUMBER: US/08/417,210A
 i FILING DATE: 05-APR-1995
 i CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 i NAME: KOWALSKI, THOMAS J.
 i REGISTRATION NUMBER: 32,147
 i REFERENCE/DOCKET NUMBER: 454310-26690
 i TELECOMMUNICATION INFORMATION:
 i TELEPHONE: 212-840-3333
 i INFORMATION FOR SEQ ID NO: 115:
 i SEQUENCE CHARACTERISTICS:
 LENGTH: 2020 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-417-210A-135
 Query Match Score 90; DB 2; Length 2020;
 Best Local Similarity 100.0%; Prod. No. 5.4e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAAATAATCAGGACTTGTGGAGATGGGGTGGAGATGGGGACCATG 60
 Db 297 ATGAGAGTGAAGGAAATAATCAGGACTTGTGGAGATGGGGTGGAGATGGGGACCATG 356

Qy 61 CTCCTGGATGTGATGATCTGTAGTGTCT 90
 Db 357 CTCCCTGGATGTGATGATCTGTAGTGTCT 386

RESULT 4
 US-08-417-210A-138
 Query Match Score 90; DB 4; Length 2020;
 Best Local Similarity 100.0%; Prod. No. 5.4e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAAATAATCAGGACTTGTGGAGATGGGGTGGAGATGGGGACCATG 60
 Db 297 ATGAGAGTGAAGGAAATAATCAGGACTTGTGGAGATGGGGTGGAGATGGGGACCATG 356

Qy 61 CTCCTGGATGTGATGATCTGTAGTGTCT 90
 Db 357 CTCCCTGGATGTGATGATCTGTAGTGTCT 386

RESULT 3
 US-09-136-159A-135
 Query Match Score 90; DB 2; Length 2020;
 Best Local Similarity 100.0%; Prod. No. 5.4e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGAGTGAAGGAAATAATCAGGACTTGTGGAGATGGGGTGGAGATGGGGACCATG 60
 Db 297 ATGAGAGTGAAGGAAATAATCAGGACTTGTGGAGATGGGGTGGAGATGGGGACCATG 356

Qy 61 CTCCTGGATGTGATGATCTGTAGTGTCT 90
 Db 357 CTCCCTGGATGTGATGATCTGTAGTGTCT 386

RESULT 3
 US-09-136-159A-135
 Patent No. 6596279
 GENERAL INFORMATION:
 APPLICANT: Virogenetics Corporation
 APPLICANT: Paoletti, Enzo
 APPLICANT: Tarraglia, James S
 APPLICANT: Cox, William I.
 i TITLE OF INVENTION: Immuno deficiency recombinant poxvirus
 i FILE REFERENCE: 454310-2660.1
 i CURRENT APPLICATION NUMBER: US/09/136,159A

Computer readable form:
 Medium type: Floppy disk
 Computer: IBM PC compatible
 Operating system: PC-DOS/MS-DOS
 Software: Patentn Release #1.0. Version #1.30
 Current application data:
 Application number: US/08/417,210A
 Filing date: 05-APR-1995
 Classification: 435
 Attorney/agent information:
 Name: Kowalski, Thomas J.
 Registration number: 32,147
 Reference/docket number: 454310-26690
 Telephone: 212-840-3333

INFORMATION FOR SEQ ID NO: 138:

SEQUENCE CHARACTERISTICS:
 LENGTH: 2028 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

RESULT 6
 US-08-417-210A-141 ; Sequence 141, Application US/08417210A
 ; Patent No. 5663542 ; GENERAL INFORMATION:
 ; APPLICANT: PAOLETTI, ENZO
 ; APPLICANT: TARTAGLIA, JAMES I.
 ; APPLICANT: COX, WILLIAM T.
 ; TITLE OF INVENTION: IMMUNODEFICIENCY RECOMBINANT POXVIRUS
 ; NUMBER OF SEQUENCES: 148
 ; CORRESPONDENCE ADDRESS:
 ADDRESSEE: CURTIS, MORRIS & SAFFORD, P.C.
 STREET: 530 FIFTH AVENUE
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/417,210A
 FILING DATE: 05-APR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: KOWALSKI, THOMAS J.
 REGISTRATION NUMBER: 32,147
 REFERENCE/DOCKET NUMBER: 454310-2690
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-840-3333
 INFORMATION FOR SEQ ID NO: 141:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2060 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)

US-08-417-210A-141
 Query Match 100 0%; Score 90; DB 2; Length 2028;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAGAGATGAGGAAATATCGCACTGTGGAGATGGGTGGAGATGGGACCATG 60
 Db 297 ATAGAGATGAGGAAATATCGCACTGTGGAGATGGGTGGAGATGGGACCATG 356

Qy 61 CTCCCTGGGATGTGATCTGATCTAGTCT 90
 Db 357 CTCCCTGGGATGTGATCTGATCTAGTCT 386

RESULT 5
 US-09-136-159A-138 ; Sequence 138, Application US/09136159A
 ; GENERAL INFORMATION:
 ; APPLICANT: Virogenetics Corporation
 ; APPLICANT: Paoletti, Enzo
 ; APPLICANT: Tartaglia, James
 ; APPLICANT: Cox, William I.
 ; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
 ; FILE REFERENCE: 454310-2690.1
 ; CURRENT APPLICATION NUMBER: US/09/136,159A
 ; CURRENT FILING DATE: 1998-08-14
 ; PRIOR APPLICATION NUMBER: US 08/417,210
 ; PRIOR FILING DATE: 1995-04-05
 ; PRIOR APPLICATION NUMBER: US 08/223,842
 ; PRIOR FILING DATE: 1994-04-06
 ; PRIOR APPLICATION NUMBER: US 07/897,382
 ; PRIOR FILING DATE: 1992-06-11
 ; PRIOR APPLICATION NUMBER: US 07/715,921
 ; PRIOR FILING DATE: 1993-08-12
 ; PRIOR APPLICATION NUMBER: US 08/105,483
 ; PRIOR FILING DATE: 1992-03-06
 ; PRIOR APPLICATION NUMBER: US 07/847,951
 ; PRIOR FILING DATE: 1991-06-11
 ; PRIOR APPLICATION NUMBER: US 07/666,056
 ; PRIOR FILING DATE: 1991-03-07
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 138
 ; LENGTH: 2028
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Nucleotide sequence of H6-promoted HIV1 SP120 + TM (with ELDKWA e OTHER INFORMATION: pitopes) gene between 14L flanking arms, coding strand.

US-09-136-159A-138
 Query Match 100.0%; Score 90; DB 4; Length 2028;
 Best Local Similarity 100.0%; Pred. No. 5.4e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATAGAGATGAGGAAATATCGCACTGTGGAGATGGGTGGAGATGGGACCATG 60
 Db 297 ATAGAGATGAGGAAATATCGCACTGTGGAGATGGGTGGAGATGGGACCATG 356

Qy 61 CTCCCTGGGATGTGATCTGATCTAGTCT 90
 Db 357 CTCCCTGGGATGTGATCTAGTCT 386

RESULT 7
 US-09-136-159A-141 ; Sequence 141, Application US/09136159A
 ; Patent No. 6506279 ; GENERAL INFORMATION:
 ; APPLICANT: Virogenetics Corporation
 ; APPLICANT: Paoletti, Enzo
 ; APPLICANT: Tartaglia, James
 ; TITLE OF INVENTION: Immunodeficiency recombinant poxvirus
 ; FILE REFERENCE: 454310-2690.1
 ; CURRENT APPLICATION NUMBER: US/09/136,159A
 ; CURRENT FILING DATE: 1998-08-14
 ; PRIOR APPLICATION NUMBER: US 08/417,210
 ; PRIOR FILING DATE: 1995-04-05
 ; PRIOR APPLICATION NUMBER: US 08/223,842
 ; PRIOR FILING DATE: 1994-04-06

PRIOR APPLICATION NUMBER: US 07/897,382
 PRIOR FILING DATE: 1992-06-11
 PRIOR APPLICATION NUMBER: US 07//715,921
 PRIOR FILING DATE: 1991-06-14
 PRIOR APPLICATION NUMBER: US 08/105,483
 PRIOR FILING DATE: 1993-08-12
 PRIOR APPLICATION NUMBER: US 07/847,951
 PRIOR FILING DATE: 1992-03-06
 PRIOR FILING DATE: 1991-06-11
 PRIOR FILING DATE: US 07//666,056
 NUMBER OF SEQ ID NOS: 149
 SEQ ID NO: 141
 LENGTH: 2060
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Hs-promoted HIV1 gp120 + TM (with ELDKWA epitopes) gene between A
 OTHER INFORMATION: 24R and K11 flanking arms, coding sequence
 US-09-136-159A-141

Query Match 100.0%; Score 90; DB 4; Length 2060;
 Best Local Similarity 100.0%; Pred. No. 5 4e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGGAGGAAATACTGGACTTGGAATGGGGTGGAGATGGGGACCATG 60
 Db 297 ATGAGATGGAGGAAATACTGGACTTGGAATGGGGTGGAGATGGGGACCATG 356
 Qy 61 CTCCTGGATGTGATGATCTGTAGCT 90
 Db 357 CTCCCTGGATGTGATGATCTGTAGCT 386

RESULT 8
 US-07-916-098A-1
 Sequence 1, Application US/07916098A
 Patent No. 5871732
 GENERAL INFORMATION:
 APPLICANT: BURKLY, LINDA C.
 APPLICANT: CHISHOLM, PATRICIA L.
 APPLICANT: THOMAS, DAVID W.
 APPLICANT: ROSA, MARGARET D.
 APPLICANT: ROSA, JOSEPH J.
 TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
 TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
 STREET: 10 SOUTH WACKER DRIVE
 CITY: CHICAGO
 STATE: ILLINOIS
 COUNTRY: U.S.A.
 ZIP: 60606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/916,098A
 FILING DATE: July 24, 1992
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/08843
 FILING DATE: NO. 5871732ember 27, 1991
 CLASSIFICATION: 424
 APPLICATION NUMBER: 07/618,542
 FILING DATE: NO. 5871732ember 27, 1990
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:

NAME: JOHN J. MC DONNELL
 REGISTRATION NUMBER: 26,949
 REFERENCE/DOCKET NUMBER: 92,310-G
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (312) 715-1000
 TELEX: (312) 715-1234
 TELEX: 910/221-5317
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 251 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FEATURE:
 NAME/KEY: sig_peptide
 LOCATION: 1...87
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: 88..2568
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1533..1534
 OTHER INFORMATION: /note= "gp120/gp41 cleavage site"
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1...2568
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1
 OTHER INFORMATION: /note= "pre-HIV gp160"
 US-07-916-098A-1

Query Match 100.0%; Score 90; DB 2; Length 2571;
 Best Local Similarity 100.0%; Pred. No. 5.8e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGGAGGAAATACTGGACTTGGAATGGGGTGGAGATGGGGACCATG 60
 Db 1 ATGAGATGGAGGAAATACTGGACTTGGAATGGGGTGGAGATGGGGACCATG 60
 Qy 61 CTCCCTGGATGTGATGATCTGTAGCT 90
 Db 61 CTCCCTGGATGTGATGATCTGTAGCT 90

RESULT 9
 US-08-147-890-1
 Sequence 1, Application US/08147890
 Patent No. 5714116
 GENERAL INFORMATION:
 APPLICANT: Weiner, David
 APPLICANT: Williams, William
 APPLICANT: Levy, David N.
 TIME OF INVENTION: Chimeric Envelope Proteins for Viral
 NUMBER OF SEQUENCES: 20
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Howson and Howson
 STREET: Spring House Corporate Cntr, P.O. Box 457
 CITY: Spring House
 STATE: Pennsylvania
 COUNTRY: USA
 ZIP: 19477
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORD PERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/916,098A
 FILING DATE: July 24, 1992
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/08843
 FILING DATE: NO. 5871732ember 27, 1991
 CLASSIFICATION: 424
 APPLICATION NUMBER: 07/618,542
 FILING DATE: NO. 5871732ember 27, 1990
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: US/08/147,890

FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/718,537
 FILING DATE: 21-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Pak, Mary E.
 REGISTRATION NUMBER: 31,215
 REFERENCE/DOCKET NUMBER: WST15AUSA
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 215-540-9400
 INFORMATION FOR SEQ ID NO: 1:
 LENGTH: 2694 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (Genomic)
 US-08-147-890-1

Query Match 100.0% Score 90; DB 1; Length 2694;
 Best Local Similarity 100.0% Pred. No. 5.9e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGAAAGGAATAATCAGCACTGTGGAGATGGGGCACATG 60
 Db 271 ATGAGATGAAAGGAATAATCAGCACTGTGGAGATGGGGCACATG 330

Qy 61 CTCCTTGGATGTGATGCTGTAGTGT 90
 Db 331 CTCCTTGGATGTGATGCTGTAGTGT 360

RESULT 10
 US-09-125-131B-1
 Sequence 1, Application US/09325131B
 PARENT NO. 6492104
 GENERAL INFORMATION:
 APPLICANT: CLOUD, MILES W.
 INVENTION: EIA TEST USING NONDENATURED HIV ANTIGEN FOR EARLY DETECTION OF HIV INFECTION
 FILE REFERENCE: UTSG:224
 CURRENT APPLICATION NUMBER: US/09/325.131B
 CURRENT FILING DATE: 1999-06-08
 PRIOR APPLICATION NUMBER: 08/728,122
 PRIOR FILING DATE: 1996-10-19
 PRIOR APPLICATION NUMBER: 08/143,168
 PRIOR FILING DATE: 1993-10-26
 NUMBER OF SEQ ID NOS: 1
 SEQ ID NO 1
 LENGTH: 2696
 TYPE: DNA
 ORGANISM: Homo sapiens
 US 09-325-131B-1

Query Match 100.0% Score 90; DB 4; Length 2696;
 Best Local Similarity 100.0% Pred. No. 5.9e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGATGAAAGGAATAATCAGCACTGTGGAGATGGGGCACATG 60
 Db 440 ATGAGATGAAAGGAATAATCAGCACTGTGGAGATGGGGCACATG 499

Qy 61 CTCCTTGGATGTGATGCTGTAGTGT 90
 Db 500 CTCCTTGGATGTGATGCTGTAGTGT 529

RESULT 11
 US-08-728-122-1
 Sequence 1, Application US/08728122-1
 PARENT NO. 5462872
 APPLICANT: Trulli, Stephen
 INVENTION: HUMAN LYMPHOID CELLS EXPRESSING HUMAN IMMUNODEFICIENCY VIRUS ENVELOPE PROTEIN GP160
 NUMBER OF SEQUENCES: 1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/134.128
 FILING DATE: 08-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 906,613
 FILING DATE: 30-JUN-1992
 APPLICATION NUMBER: 587,011
 FILING DATE: 24-SEP-1990
 SEQ ID NO:1
 LENGTH: 2945

RESULT 11
 US-08-728-122-1

Query Match 100.0%; Score 90; DB 1; Length 2945;
 Best Local Similarity 100.0%; Pred. No. 6e-21; Indels 0; Gaps 0;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGGTGAGGAGAAATTCGACATTGGAGATGGGGTGGAGATGGGCCACATG 60

Db 268 ATGAGGTGAGGAGAAATTCGACATTGGAGATGGGGTGGAGATGGGCCACATG 327

Qy 61 CTCCCTGGGATGTTGATGACTCTGAGTCGTAGTGCCT 90

Db 328 CTCCCTGGGATGTTGATGACTCTGAGTCGTAGTGCCT 357

RESULT 13 US-08-147-890-2

Sequence 2, Application US/08147890

Patent No. 5714316

GENERAL INFORMATION:

APPLICANT: Weiner, David

APPLICANT: Williams, William

APPLICANT: Levy, David N.

TITLE OF INVENTION: Chimeric Envelope Proteins for Viral

TITLE OF INVENTION: Targeting

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr, P.O. Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/147,890

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/718,537

FILING DATE: 21-JUN-1991

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST15USA

TELEPHONE: 215-540-5818

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 3084 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: unknown

MOLECULE TYPE: DNA (genomic)

US-08-147-890-2

Score 90; DB 3; Length 3563;

Best Local Similarity 100.0%; Pred. No. 6.4e-21;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGGTGAGGAGAAATTCGACATTGGAGATGGGGTGGAGATGGGCCACATG 60

Db 271 ATGAGGTGAGGAGAAATTCGACATTGGAGATGGGGTGGAGATGGGCCACATG 330

Qy 61 CTCCCTGGATGTTGATGACTCTGAGTCGTAGTGCCT 90

Db 331 CTCCCTGGATGTTGATGACTCTGAGTCGTAGTGCCT 360

RESULT 15 US-08-463-210-6

Sequence 6, Application US/08463028

Patent No. 6610476

US-08-463-210-6

Application US/08463210

Patent No. 6001977

GENERAL INFORMATION:

APPLICANT: CHANG, Nancy T.

APPLICANT: GALLO, Robert C.

APPLICANT: WONG-STAAI, Flossie

TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morgan & Finnegan, L.L.P.

STREET: 345 Park Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10154-0053

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/463,210

FILING DATE: 05-JUN-1995

CLASSIFICATION: 436

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/693,866

FILING DATE: 23-JAN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 06/659,339

FILING DATE: 10-OCT-1984

ATTORNEY/AGENT INFORMATION:

NAME: Serurian, Leslie A.

REGISTRATION NUMBER: 35,353

REFERENCE/DOCKET NUMBER: 2026-4193US2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 758-4800

TELEFAX: (212) 751-6849

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 3563 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: HTLV-III

FEATURE:

NAME/KEY: misc_feature

LOCATION: 1..3563

OTHER INFORMATION: /standard name= "Clone BH8"

/note= "Corresponds to nucleotide positions 5580

/OTHER INFORMATION: to 9154 in figure 3 of US 06/693,866"

US-08-463-210-6

Query Match 100.0%; Score 90; DB 3; Length 3563;

Best Local Similarity 100.0%; Pred. No. 6.4e-21;

Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGAGGTGAGGAGAAATTCGACATTGGAGATGGGGTGGAGATGGGCCACATG 60

Db 226 ATGAGGTGAGGAGAAATTCGACATTGGAGATGGGGTGGAGATGGGCCACATG 285

Qy 61 CTCCCTGGATGTTGATGACTCTGAGTCGTAGTGCCT 90

Db 286 CTCCCTGGATGTTGATGACTCTGAGTCGTAGTGCCT 315

RESULT 15 US-08-463-028-6

Sequence 6, Application US/08463028

Patent No. 6610476

RESULT 14

GENERAL INFORMATION:

APPLICANT: CHANG, Nancy T.
 APPLICANT: GALLO, Robert C.
 APPLICANT: WONG-STAAI, Flossie
 TITLE OF INVENTION: CLONING AND EXPRESSION OF HTLV-III DNA
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morgan & Finnegar, L.L.P.
 STREET: 345 Park Avenue
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10154-0053
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/01/463,028
 FILING DATE: 05-JUN-1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/693,866
 FILING DATE: 23-JAN-1985
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 06/659,339
 FILING DATE: 10-OCT-1984
 ATTORNEY/AGENT INFORMATION:
 NAME: Serunian, Leslie A.
 REGISTRATION NUMBER: 35,353
 REFERENCE/DOCKET NUMBER: 2026-4193US3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 758-4800
 TELEFAX: (212) 751-6849
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 3563 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ORIGINAL SOURCE:
 ORGANISM: HTLV-III
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..3563
 OTHER INFORMATION: /standard name="Clone BH8"
 OTHER INFORMATION: /note="Corresponds to nucleotide positions 5580
 OTHER INFORMATION: to 9154 in Figure 3 of US 06/693,866"
 US-08-463-028-6

Query Match 100.0%; Score 90; DB 4; Length 3563;
 Best Local Similarity 100.0%; Pred. No. 6.4e-21;
 Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ATAGAGTAAGGAAATAGCACTGTGATCATCTGAGTC
 Db 226 ATAGAGTAAGGAAATAGCACTGTGATCATCTGAGTC 90
 QY 61 CTCCCTGGATGTGATGATCTGAGTCAGTGTGCT 315
 Db 286 CTCTTGGATGTGATGATCTGAGTCAGTGTGCT 285

Genecore version 5.1.6
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OM nucleic - nucleic search, using BW model

Run on: March 11, 2004, 19:37:35 ; Search time 2481.77 Seconds
 Perfect score: 129 (without alignments)
 Sequence: 1 ttattccatgtatggatagg.....acctcccaatcccgaaaa 129
 1552.207 Million cell updates/sec

Title: US-10-003-035-75
 Scoring table: IDENTITY_NUC
 Gapox 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578
 Minimum DB seq length: 0
 Maximum DB seq length: 20000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_estbm:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estsco:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estom:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_tun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_pr1:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	79	61.2	145	AB036493	AB036493 mRNA linear CJ7 145 bp
2	70	54.3	232	XBB8515	XBB8515 H. sapiens D
3	37.4	29.0	110	CG788669	CG788669 ZMBB024
4	35.8	27.8	816	CG453676	CG453676 OGYGU63TH

DEFINITION

AB036493	Mus musculus	CJ7 brain, liver, kidney, lung, heart
LOCUS	CDNA clone	mRNA sequence.
DEFINITION		
VERSION	EST.	
KEYWORDS		
SOURCE	Mus musculus (house mouse)	
ORGANISM		
REFERENCE	1 (bases 1 to 145)	
AUTHORS	Wang, Y.L., Saigoh, K., Osaka, H., Yamashita, T., Suh, J.G.,	
TITLE	Kiyosawa, H., Sakai, Y., Wakana, S. and Wada, K.	
COMMENT	YAC/BAC-based physical and transcript mapping around the gracile axonal dyrophy (gad) locus identifies uchII, Pnx2b, atpaa2, and	
JOURNAL	Genomics 66 (3), 333-336 (2000)	
MEDLINE	20334630	
PUBLMED	10873389	

ALIGNMENTS

RESULT 1	AB036493	Mus musculus	CJ7 brain, liver, kidney, lung, heart
LOCUS	AB036493	CDNA clone	mRNA sequence.
DEFINITION			
ACCESSION	AB036493		
VERSION	EST.		
KEYWORDS			
SOURCE	Mus musculus (house mouse)		
ORGANISM			
REFERENCE	1 (bases 1 to 145)		
AUTHORS	Wang, Y.L., Saigoh, K., Osaka, H., Yamashita, T., Suh, J.G.,		
TITLE	Kiyosawa, H., Sakai, Y., Wakana, S. and Wada, K.		
COMMENT	YAC/BAC-based physical and transcript mapping around the gracile axonal dyrophy (gad) locus identifies uchII, Pnx2b, atpaa2, and		
JOURNAL	Genomics 66 (3), 333-336 (2000)		
MEDLINE	20334630		
PUBLMED	10873389		

clones (414D20, 220F19, Research Genetics) using exon trapping method.

FEATURES

source

1. .145
/organism="Mus musculus"
/mol_type="mRNA"
/strain="129/Sv"
/db_xref="taxon:10090"
/mP= "5"
/clone="115-5"
/sex="male"
/tissue type="brain liver kidney lung heart"
/cell_line="C07 embryonic stem cell line"
/dev_stage="adult"
/clone_lib="Mus musculus C07 brain, liver, kidney, lung, heart"

ORIGIN

Query Match
Best Local Similarity 61.2%;
Matches 100; **Conservative** 88.5%;
Score 79; **DB** 9; **Length** 145;
Pred. No. 3.2e-13;
Indels 8; **Gaps** 1;
0; **Mismatches** 5;
Source Zea mays subsp. mays (maize)

ACCESSION X88515
VERSION X88515.1
KEYWORDS ORGANISM Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophytina; Magnoliidae; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J.

AUTHORS and Wing, R.

TITLE Sequencing of the maize genome

JOURNAL Unpublished (2000)

COMMENT Contact: Rod Wing

ORIGIN

RESULT 2
LOCUS HSMC01D05
DEFINITION H.sapiens DNA for trapped exon (ID HMC01D05), genomic survey sequence.
ACCESSION X88515
VERSION X88515.1
KEYWORDS SOURCE Homo sapiens (human)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE Chen, H., Chrust, R., Rossier, C., Morris, M.A., Lalotti, M.D. and Antonarakis, S.E.
TITLE Cloning of 559 potential exons of genes of human chromosome 21 by exon trapping
JOURNAL Genome Res. 6 (8), 747-760 (1996)
MEDLINE 97011340
PUBMED 8888350
REFERENCE Chen, H.M., Rossier, C., Chrust, R. and Antonarakis, S.E.
TITLE Cloning of trapped exons from human chromosome 21
JOURNAL
REFERENCE 3 (bases 1 to 232)
AUTHORS Antonarakis, S.E.
TITLE Direct Submission
JOURNAL Submitted (17-MAR-1995) Stylianos E. Antonarakis, Division of Medical Genetics, University and Cantonal Hospital of Geneva, CMU, 1 rue Michel Servet, 1211 Geneva, SWITZERLAND

ORIGIN

Query Match 29.0%; **Score** 37.4; **DB** 29; **Length** 110;
Best Local Similarity 64.4%; **Pred.** No. 0.84;
Matches 56; **Conservative** 0; **Mismatches** 31; **Indels** 0; **Gaps** 0;
Source Zea mays subsp. mays (maize)
Location/Qualifiers 1..232
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
exon
1..232
/note="trapped exon"

RESULT 4
LOCUS CG453676
DEFINITION ZMMBBD0243B19-3, genomic survey sequence.

Query Match 110 bp; **Score** 70; **DB** 29; **Length** 232;
Best Local Similarity 86.4%; **Pred.** No. 1.7e-10;
LOCUS CG453676

DEFINITION ZMMBBD0243B19-3, genomic survey sequence.

DEFINITION CGVGU63TH ZM_0_7_1.5_KB Zea mays genomic clone ZMMBMA0479K05 ,
 genomic survey sequence.

ACCESSION CG453676 GI : 348338676

KEYWORDS GSS .

SOURCE Zea mays

ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade: Panicoideae; Andropogoneae; Zea .

REFERENCE White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Numberg, A.N., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)

JOURNAL Contact: Cathy White,law

COMMENT TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: white,law@tigr.org
 Seq primer: TR
 Class: sheared ends.

FEATURES source

ORIGIN

Query Match 27.8%; Score 35.8; DB 29; Length 816;
 Best Local Similarity 63.2%; Pred. No. 3.3; Indels 0; Gaps 0;
 Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Query 4 TTCAAATAGTAGGAGGCCTGGTAGTTTAAAGATAGTTTGCTGTCTCGTA 63
 Db 525 TTATAAATAATAGGTGATGTTAGTTAGTTAAAGCATTTAACGATTA 584

Query 64 GTGATAGTTAGGCTAGCAGGATATTCA 90
 Db 645 GTTAAAGTATTAGTTCTGGATTTC 611

RESULT 5

LOCUS CG453685_c 851 bp DNA linear GSS 17-SEP-2003

DEFINITION CGVGU63TV ZM_0_7_1.5_KB Zea mays genomic clone ZMMBMA0479K05 ,
 genomic survey sequence.

ACCESSION CG453685

VERSION CG453685.1 GI : 348338685

KEYWORDS GSS .

SOURCE Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade: Panicoideae; Andropogoneae; Zea .

REFERENCE White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Numberg, A.N., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)

JOURNAL Contact: Cathy White,law

COMMENT TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843
 Fax: 301-838-0208
 Email: white,law@tigr.org
 Seq primer: TR
 Class: sheared ends.

FEATURES source

ORIGIN

Query Match 27.8%; Score 35.8; DB 29; Length 851;
 Best Local Similarity 63.2%; Pred. No. 3.3; Indels 0; Gaps 0;
 Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Query 4 TICATAATGATAGTAGGAGGCTGGTGGTTAAAGATAAGTTTGCTGTACTTCGTA 63
 Db 705 TTAATTAATAATAGCTGATGATTTCAGTTAAATAGGATTTTAAGGATTAAAGTAAAGTA 646

Query 64 GTCATAGTGGATTTAGTCTGGATTCA 90
 Db 645 GTTAAAGTATTAGTTCTGGATTTC 619

RESULT 6

LOCUS CG416525 936 bp DNA linear GSS 22-SEP-2003

DEFINITION ZMMBBC0024C16E ZMMBBC (ECORI) Zea mays subsp. mays genomic clone ZMMBBC0024C16_5 , genomic survey sequence.

ACCESSION CG416525

VERSION CG416525.1 GI : 34561370

KEYWORDS GSS .

SOURCE Zea mays subsp. mays (maize)

ORGANISM Zea mays subsp. mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade: Panicoideae; Andropogoneae; Zea .

REFERENCE 1 (bases 1 to 936)
 Bharti, A.K., Young, S., Kavchik, S., Keizer, G., Bronzino, A.C.,
 Zohovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.
 Sequencing of the maize genome at PGIR (2003c)
 Unpublished (2003)
 Contact: Bharti, A.K.
 Dr.Joachim Messing's lab
 The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
 University
 190 Frelinghuysen Road, Piscataway, NJ 08854, USA
 Tel: 732 445 3801
 Fax: 732 445 5735
 Email: bharti@waksman.rutgers.edu
 Seq primer: T7

Class: BAC ends

High quality sequence start: 79 .
 Location/Qualifiers

FEATURES source

ORIGIN

Query Match 27.8%; Score 35.8; DB 29; Length 851;
 Best Local Similarity 63.2%; Pred. No. 3.3; Indels 0; Gaps 0;
 Matches 55; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

Query 4 TTCAAATAGTAGGAGGCCTGGTAGTTTAAAGATAGTTTGCTGTCTCGTA 63
 Db 525 TTATAAATAATAGGTGATGTTAGTTAGTTAAAGCATTTAACGATTA 584

Query 64 GTGATAGTTAGGCTAGCAGGATATTCA 90
 Db 645 GTTAAAGTATTAGTTCTGGATTTC 611

RESULT 5

LOCUS CG453685_c 851 bp DNA linear GSS 17-SEP-2003

DEFINITION CGVGU63TV ZM_0_7_1.5_KB Zea mays genomic clone ZMMBMA0479K05 ,
 genomic survey sequence.

ACCESSION CG453685

VERSION CG453685.1 GI : 348338685

KEYWORDS GSS .

SOURCE Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 Clade: Panicoideae; Andropogoneae; Zea .

REFERENCE 1 (bases 1 to 851)
 White, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Numberg, A.N., Robbins, D. and Lakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)

JOURNAL Contact: Cathy White,law

COMMENT TIGR
 Other_GSS: OGVGU63TV

ORIGIN

Query Match 27.8%; Score 35.8; DB 29; Length 936;

Best Local Similarity	63.2%	Pred. No.	3.4	SOURCE	Zea mays
Matches	55; Conservative	0; Mismatches	32;	Indels	0; Gaps 0;
Qy	4 TTCATAATGATAGGGCTTGTAGTTTAAGATAATGTTTGCTGTA 63	DEFINITION	Zea mays; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD		
Db	649 TTAAATAAAATAGTTCAATGTTTAAGGCAATTAAAGTA 708	REFERENCE	1 (bases 1 to 782)		
Qy	64 GTGAAATAGGTAGCCAGGGATATTCA 90	AUTHORS	Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenberger, P., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martienssen, R.A.		
Db	709 GTAAAAGGTAGTTATGGATTAA 735	TITLE	Genomic shotgun sequences from Zea mays (methyl-filtered)		
		JOURNAL	Unpublished (2002)		
		COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874 Email: mccombie@cshl.org		
RESULT	7	ORGANISM	Zea mays		
CG019434/C	CG019434	LOCUS	270 bp	FEATURES	DNA
DEFINITION	ZUAFN74H 2M 3.0 4.0 KB	LINEAR	GSS 19-AUG-2003		
GENOMIC SURVEY	SEQUENCE	SOURCE	Zea mays genomic clone ZMBP0052N04,		
ACCESSION	CG019434	ORGANISM	Zea mays		
VERSION	CG019434.1	NAME	GI:33891599		
KEYWORDS		FEATURES	Organism=Zea mays		
SOURCE		LOCATION/QUALIFIERS	/mol_type="genomic DNA"		
ORGANISM		1.	/db_xref="taxon:4577"		
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; clade; Panicoideae; Andropogoneae; Zea.		2.	/clone="IR30C12"		
Bacteria; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD		3.	/lab_host="DH5a"		
clade; Panicoideae; Andropogoneae; Zea.		4.	/note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (x/y reads in M13mp19, b/g reads in PUC19). The same ligation was transformed into DH5a."		
REFERENCE	1. (bases 1 to 270)	ORIGIN			
AUTHORS	Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.	QUERY MATCH	26.5%		
TITLE	Unpublished (2002)	BEST LOCAL SIMILARITY	62.1%		
JOURNAL	Other GSS: ZUAFN4TV	PRD. NO.	9.9		
COMMENT	9712 Medical Center Drive, Rockville, MD 20850, USA	MISMATCHES	0;		
	Phone: 301-838-5843	INDELS	33;		
	Fax: 301-838-0208	GAPS	0;		
	Email: white.law@igr.org				
SEG PRIMER: TR	CLASS: sheared ends				
	LOCATION/QUALIFIERS				
	1.				
FEATURES	1.270				
SOURCE	/organism="Zea mays"				
	/mol_type="genomic DNA"				
	/strain="B73"				
	/db_xref="taxon:4577"				
	/clone="ZUMBP0052N04"				
	/clone.lib="2M 3.0 4.0 KB"				
	/note="Vector: pBGSK; Site_1: HinClI; 3-4 kb 'unfiltered'				
	genomic DNA library"				
ORIGIN					
	Query Match	Score	34.2;		
	Best Local Similarity	DB	28;		
	Matches	Length	782;		
	54; Conservative				
	0; Mismatches				
	33; Indels				
	0; Gaps				
RESULT	9	DEFINITION	BH332797 CH23-0-5917.TJ CHORI-230 Segment 1 Ratnus norvegicus genomic clone		
BH332797	LOCUS	ACCESSION	BH332797 BH332797_1, Genomic survey sequence.		
CH23-0-5917	DEFINITION	KEYWORDS	GSS.		
CH23-0-5917, Genomic survey sequence.	DEFINITION	ORGANISM	Rattus norvegicus (Norway rat)		
	DEFINITION	ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butherzia; Rodentia; Sciurognathi; Muridae; Murinae;		
	DEFINITION	ORGANISM	Rattus norvegicus (Norway rat)		
REFERENCE	1 (bases 1 to 794)	REFERENCE	Zhao, S., Shetty, J., Shatsman, S., Tsugaya, G., Geer, K., Shavtsev, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, P., de Jong, P. and Fraser, C.M.		
AUTHORS		TITLE	Rat BAC End Sequences from Library CHORI-230 EcoRI segment		
		JOURNAL	Unpublished (1999)		
RESULT	8	DEFINITION	CC167485 CC167485 DNA linear GSS 29-APR-2003		
CC167485	LOCUS	DEFINITION	782 bp (DH5a methyl filtered) Zea mays genomic clone		
DEFINITION	ik30c12.92	DEFINITION	ik30c12, genomic survey sequence.		
ACCESSION	CC167485	DEFINITION	CC167485		
VERSION	CC167485.1	DEFINITION	CC167485.1 GI:30199003		
KEYWORDS		DEFINITION			

COMMENT	FEATURES source	FEATURES source	LOCATION/QUALIFIERS
Other_GSSs: CH230-5917.TV Contact: Shaying Zhao The Institute of Eukaryotic Genomics 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301-838-0200 Fax: 301-838-0208 Email: szhao@tigr.org			1. -805 /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="BAXON:4577" /clone="ZMMBPA0052N03" /clone_libr="ZM 3.0 4.0 KB" /note="vector: PBCSK; Site 1: HincII; 3-4 kb 'unfiltered' genomic DNA library"
Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end Plate: 59 row: I column: 7 Seq primer: SP6 Class: BAC ends.			
FEATURES source	Location/Qualifiers 1. -794 /organism="Rattus norvegicus" /mol_type="genomic DNA" /strain="BN/SNHsd/MCW" /db_xref="taxon:10167" /clone="CH230-5917" /sex="Female" /clone_type="Brain" /clone_libr="CHORI-230 Segment 1" (note="vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI; CHORI-230 Rat (BN/SNHsd/MCW) BAC library produced by Pieter de Jong")		
ORIGIN			
Query Match Score 34.2%; DB 28; Length 794; Best Local Similarity 62.1%; Pred. No. 10; Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;			
Qy 8 TAATGATACTAGGGGCTGTAGGTTAAGAAATAGTTTGCTGTACTTCCTGTAAGCA 67 Db 532 TTATATGATGGATTGATCAGGACAGGAGAATGGTTTCCTCCCTTATCGCTTA 591			
Query Match Score 34.2%; DB 28; Length 794; Best Local Similarity 62.1%; Pred. No. 10; Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;			
Qy 68 ATAGAGTTAGCAGGGATATTCCACAT 94 Db 592 ACACGGTTATGCTACTACACTCACCAT 618			
RESULT 10 LOCUS CC986340/C 805 bp DNA linear GSS 18-AUG-2003 DEFINITION genomic survey sequence. ACCESSION-VERSION CC986340 KEYWORDS GSS. SOURCE Zea mays ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; PACCAD clade; Panicoideae; Andropogoneae; Zea. 1. (bases 1 to 805) White, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002)			
REFERENCE AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Bedell, J.A., Rohlfing, T., Citek, R.W., Numberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002)			
JOURNAL COMMENT Contact: Cathy Whitelaw			
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TR Class: sheared ends.			
ORIGIN			
Query Match Score 34.2%; DB 29; Length 807; Best Local Similarity 62.1%; Pred. No. 10; Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;			
Qy 4 TTCAATATGATAGGGGCTGTAGGTTAAGAAATAGTTTGCTGTACTTCCTGTA 63 Db 660 TTAATAAAATAGTTCATGGTTTATGGTAAATAGGGATTTAGGTATTAAGTA 719			

Qy 64 GTCAATAGGTAGGCCAGGGATATTCA 90
 Db 720 GTTAAACGTTAGTTCTGGATTTTA 746

RESULT 12
 CG464137/C CG464137 935 bp DNA linear GSS 17-SEP-2003
 LOCUS DEFINITION genomic clone ZMBBPA0070F22,
 Genomic survey sequence.
 ACCESSION CG464137
 VERSION GI:3484937
 KEYWORDS GSS.
 SOURCE zea mays
 ORGANISM Eukaryota; Viridiplanteae; Streptophytina; Embryophytina; Tracheophytina;
 Spermatophytina; Magnoliophytina; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE White-law, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
 Citek, R.W., Nurnberg, A., Robbins, D. and Leakey, N.
 Consortium for Maize Genomics
 Unpublished (2002)

AUTHORS Other GSSs: ZUARN35TH
 Contact: Cathy White-law
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843
 Fax: 301-838-0208
 Email: white-law@tigr.org

JOURNAL COMMENT

FEATURES source
 Class: sheared ends.
 Location/Qualifiers 1..935
 /organism="Zea mays"
 /mol type="genomic DNA"
 /strain="B73"
 /db_xref="TAXON:4577"
 /clone_lib="ZM 3.0.4.0 KB"
 /note="Vector: PBSK;-Site_1: HincII; 3-4 kb 'unfiltered'
 genomic DNA library"

ORIGIN Query Match Score 34.2; DB 13; Length 935;
 Best Local Similarity 62.1%; Pred. No. 10;
 Matches 54; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

Qy 4 TICATAATGATAGTAGGGCGGTGGTAGTTTAAGAATAGTTCTGACTTTCTGTA 63
 Db 348 TAATAAAAATAGTTGTGATTTAGTTAATAGGAATTCTAGGCCTTTAACATA 289

Qy 64 GTGAATAGAGTTAGGGCAGGGATTCA 90
 Db 288 GTTAAAACCTTATGTTAGGATTATA 262

RESULT 13
 BQ098469 BQ098469 513 bp mRNA linear EST 20-DEC-2002
 DEFINITION phi8c07.Y12 Ostertagia ostertagi L3 pAMP1 v1 Ostertagia ostertagi
 /contains Alu repetitive element;, mRNA sequence.
 ACCESSION BQ098469
 VERSION BQ098469.1 GI:20131446
 KEYWORDS EST.
 ORGANISM Ostertagia ostertagi
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyliida;
 Trichostomylidae; Haemonchidae; Ostertaginae;
 1 (bases 1 to 513)
 REFERENCE McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J.,
 AUTHORS

Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theisinger, B.,
 Bowers, Y., Gibbons, M., Ritter, B., Bennett, J., Franklin, C.,
 Tsadarevishvili, R., Ronko, I., Kennedy, S., McGuire, J., Beck, C.,
 Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Jackson, Y.,
 Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
 McCann, R., Watsonson, R. and Wilson, R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@watson.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center
 High Quality Sequence scop: 418.

JOURNAL COMMENT

FEATURES source
 Class: sheared ends.
 Location/Qualifiers 1..513
 /organism="Ostertagia ostertagi"
 /mol type="mRNA"
 /db_xref="TAXON:6317"
 /dev_stage="L3"
 /lab_host="DH10B"
 /clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
 /note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
 ***WARNING: Subsequent examination of these samples has
 revealed the presence of an additional Trichostomylidae
 cattle nematode, Cooperia oncophora. Sequences in this
 library may derive from either Ostertagia or Cooperia.***
 The library was constructed by Claire Murphy and Dr. James
 McCarter at Washington University, St. Louis. The cDNA was
 made by using Dynabead oligo(dT) priming (Dynal). PCR based
 library using a modified protocol from the SMART PCR cDNA
 Synthesis Kit from Clontech. Directionally cloned into the
 UDG Bites of pAMP1. Nematodes were provided by Dr. Louis
 Gasbarre (louis.gasbarre@anri.barc.usda.gov). Third stage exsheathed
 larvae were collected from 14 day fecal-sphagnum moss
 cultures of Ostertagia eggs. The larvae were recovered by
 overnight passage on a Baermann apparatus, and then
 cleaned by passage through a 20 micron nylon mesh. The
 larvae were then subjected to a treatment with 1.25%
 chloro to induce excystation. The larvae were washed with
 5 changes of PBS and then pelleted and snap frozen in
 liquid nitrogen."

FEATURES source
 Class: sheared ends.
 Location/Qualifiers 1..935
 /organism="Zea mays"
 /mol type="genomic DNA"
 /strain="B73"
 /db_xref="TAXON:4577"
 /clone_lib="ZMBP0070F22"
 /note="Vector: PBSK;-Site_1: HincII; 3-4 kb 'unfiltered'
 genomic DNA library"

ORIGIN Query Match Score 33.4; DB 13; Length 513;
 Best Local Similarity 62.7%; Pred. No. 16;
 Matches 52; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

Qy 37 AGATAGTTTGCTGTACTTTCTGTAAATGAGTTAGGAGGATATTCTACCATTA 96
 Db 430 AGAAGATTCCTGATCTCATTCAGGAACTAAGTGGCTATTCTACAGGATA 489

Qy 97 TCGTTTCAGACCCACTCTCCAAAT 119
 Db 490 TTTCCTCGACACAAATGACAT 512

RESULT 14
 BQ099257 BQ099257 535 bp mRNA linear EST 20-DEC-2002
 LOCUS ph28d05_Y2_Ostertagia_ostertagi_L3_pAMP1_v1_Ostertagia_ostertagi
 DEFINITION cDNA 5' similar to SW_GCH1_OSTOS_061573 GRP CYCLOHYDROLASE I
 ; contains Alu repetitive element;, mRNA sequence.

ACCESSION BQ099257
 VERSION BQ099257.1 GI:20132241
 KEYWORDS EST.
 ORGANISM Ostertagia ostertagi
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongyliida;
 Trichostomylidae; Haemonchidae; Ostertaginae;
 1 (bases 1 to 513)
 REFERENCE McCarter, J., Clifton, S., Chiappelli, B., Pape, D., Martin, J.,
 AUTHORS

ORGANISM *Ostertagia ostertagi*
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;
Trichostyloidea; Haemonchidae; Ostertagiinae; Ostertagia.

REFERENCE 1 (bases 1 to 535)

AUTHORS McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Ritter, E., Bennett, J., Franklin, C., Bowes, Y., Dantes, M., Marra, M., Hillier, L., McGuire, L., Beck, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Pape, D., Martin, J., Ritter, E., Bennett, J., Franklin, C., Bowes, Y., Gibbons, M., Marra, M., Hillier, L., Kucaba, T., Theissing, B., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., McCann, R., Waterston, R. and Wilson, R.

TITLE Unpublished (1999)

JOURNAL The Washington Univ. Nematode EST Project, 1999

COMMENT Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center
High quality sequence stop: 419.

FEATURES source

1..535
/organism="Ostertagia ostertagi"
/mol_type="mRNA"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
/clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
/db_xref="taxon:6317"
/dev_stage="L3"
/lab_host="DH10B"

/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
/clone_lib="Ostertagia ostertagi L3 pAMP1 v1"
/note="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;
WARNING: Subsequent examination of these samples has revealed the presence of an additional Trichostrongyloidea cattle nematode, Cooperia oncophora. Sequences in this library may derive from either Ostertagia or Cooperia.
The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the TUDG sites of pAMP1. Nematodes were provided by Dr. Louis Gasbarre of the USDA, Beltsville, MD (lgasbar@ari.barc.usda.gov). Third stage exsheathed larvae were collected from 14 day fecal-sphagnum moss cultures of Ostertagia eggs. The larvae were recovered by overnight passage on a Baermann apparatus, and then cleaned by passage through a 20 micron nylon mesh. The larvae were then subjected to a treatment with 1.25% chlorox to induce excystation. The larvae were washed with 5 changes of PBS and then pelleted and snap frozen in liquid nitrogen."

ORIGIN

Query Match 25.9%; Score 33.4; DB 13; Length 535;
Best Local Similarity 62.7%; Pred. No. 16;
Matches 52; Conservative 0; Mismatches 0; Gaps 0;

Qy 37 AGAATAGTTTGCTGTACTTTCTGATAGTAGTATTGGCAGGATTCACCATTA 96
Db 430 AGAGAAATCTGAACTCATCACAGTAACTGATGCACTTCACGAGTA 489

Qy 97 TCGTTTCAGGCCACCTCCCAAT 119
Db 490 TTTTTCCGACACAATGACAAT 512

RESULT 15
B0099653 LOCUS ph33a09_y2
DEFINITION similar to SW:GCH1_OSTOS 061573 GTP CYCLOHYDROLASE I

Query Match 25.9%; Score 33.4; DB 13; Length 536;
Best Local Similarity 62.7%; Pred. No. 16;
Matches 52; Conservative 0; Mismatches 0; Gaps 0;

Qy 37 AGAAATAGTTTGCTGTACTTTCTGATAGTAGTATTGGCAGGATTCACCATTA 96
Db 431 AGAGAAATCTGAACTCATCACAGTAACTGATGCACTTCACGAGTA 490

Qy 97 TCGTTTCAGGCCACCTCCCAAT 119
Db 491 TTTTTCCGACACAATGACAAT 513

Fri Mar 12 10:05:56 2004

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Search completed: March 11, 2004, 23:09:32
Job time : 2888.1 secs



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No.	Doccode	Number of pages
1	SRNT	15

Total number of pages: 15

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